

399

```

      260      265      270
Ile Asp Val Phe Gly Asn Val Leu Glu Gly Asp Trp Asn Ser Tyr Ile
      275      280      285
Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile Val Leu Gly Ser
      290      295      300
Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp Phe Ile Asn Asn
      305      310      315      320
Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr Glu Met Met Gln
      325      330      335
Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly Gly Ser Ala Val
      340      345      350
Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser Ala Gly Gly Gly
      355      360      365
Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly Leu Gly Ala Ile
      370      375      380
Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser Val Lys Ala Gly
      385      390      395      400
Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe Gly Phe Asp Asn
      405      410      415
Asp Lys Asn Asn Lys
      420

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

```

Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1      5      10      15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
      20      25      30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
      35      40      45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
      50      55      60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
      65      70      75      80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
      85      90      95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
      100      105      110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
      115      120      125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
      130      135      140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
      145      150      155      160
Arg Arg Ser Phe Lys Unk
      165

```

400

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

```

Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1          5          10          15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
20          25          30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
35          40          45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
50          55          60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
65          70          75          80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
85          90          95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
100          105          110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
115          120          125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
130          135          140
Glu Lys Unk Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Unk Unk
145          150          155          160
Arg Arg Ser Phe Lys Unk
165

```

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

401

```

Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu Ile Arg Leu
1          5          10          15
Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr Ser Ile Ile
          20          25          30
Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp Val Leu Leu
          35          40          45
Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn Ser Ile Leu
50          55          60
Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro Thr Thr Lys
65          70          75          80
Asp Leu Leu Ala Leu Leu Lys Asp Ile
          85

```

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

```

Val Lys Thr Leu Gly Leu Ser Ser Leu Gly Gly Thr Leu Glu Phe Tyr
1          5          10          15
Asp Phe Ile Ile Phe Val Phe Phe Thr Ser Ile Ile Ala Lys His Phe
          20          25          30
Phe Pro Asn Thr Leu Ser Pro Ile Trp Ser Glu Ile Asn Thr Tyr Gly
          35          40          45
Ile Phe Ala Ala Gly Tyr Leu Ala Arg Pro Leu Gly Gly Ile Val Met
50          55          60
Ala His Phe Gly Asp Lys Phe Gly Arg Lys Asn Met Phe Met Leu Ser
65          70          75          80
Ile Leu Leu Met Val Ile Pro Thr Phe Ala Leu Ala Leu Met Pro Thr
          85          90          95
Phe Asn Asp Leu Val Gly Phe Gly Val Asp Ser Met Gly Leu Thr Pro
          100          105          110
Lys Asn Ala His Tyr Leu Gly Tyr Ile Ala Pro Val Phe Leu Val Leu
          115          120          125
Val Arg Ile Cys Gln Gly Val Ala Val Gly Gly Glu Leu Pro Gly Ala
130          135          140
Trp Val Phe Val His Glu His Ala Pro Gln Gly Gln Lys Asn Thr Tyr
145          150          155          160
Ile Gly Phe Leu Thr Ala Ser Val Val Ser Gly Ile Leu Leu Gly Ser
          165          170          175
Leu Val Tyr Ile Gly Ile Tyr Met Val Phe Asp Lys Pro Val Val Glu
          180          185          190
Asp Trp Ala Trp Arg Val Ala Phe Gly Leu Gly Gly Ile Phe Gly Ile
          195          200          205
Ile Ser Val Tyr Leu Arg Arg Phe Leu Glu Glu Thr Pro Val Phe Gln
210          215          220
Gln Met Lys Gln Gly Arg Cys Leu Ser Gln Ile Pro Ala
225          230          235

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

```

Met Arg Lys Phe Leu Asp Gly Ala Lys Ser Glu Val Leu Lys Tyr Asp
1      5      10      15
Val Ile Ser Phe Asp Ile Phe Asp Thr Leu Leu Leu Arg Pro Phe Ile
      20      25      30
Lys Pro Thr Asp Leu Phe Leu Tyr Ile Glu Thr Lys Tyr Asn Ile Lys
      35      40      45
Gly Phe His Gln Ala Arg Ile Leu Ala Glu Met Gln Ser Arg Lys Leu
      50      55      60
Ser Lys Arg Gln Asp Ile Thr Leu Asp Glu Ile Tyr His Gln Ile Pro
65      70      75      80
Lys Glu Phe His Ser Tyr Lys Gly Val Glu Ile Ala Thr Glu Lys Glu
      85      90      95
Val Leu Val Pro Asn Leu Glu Met Leu Glu Leu Tyr Arg Phe Ala Lys
      100     105     110
Glu Asn Asn Lys Arg Val Ile Ile Val Ser Asp Met Tyr Leu Pro Leu
      115     120     125
Glu Val Leu Glu Asp Ile Leu Ile Ser Lys Gly Phe Asp Gly Tyr Thr
      130     135     140
Asn Phe Tyr Leu Ser Asn His Ile Met Leu Thr Lys His Ser Lys Asp
145     150     155     160
Leu Phe Lys His Val Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile
      165     170     175
Leu His Ile Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser
      180     185     190
Leu Gly Ile Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu
      195     200     205
Glu Val Phe Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln
      210     215     220
Ser Phe Ile Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln
225     230     235     240
Lys His Glu Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala
      245     250     255
Gly Ile Ala Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His
      260     265     270
Lys Arg Asn Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu
      275     280     285
Leu Gln Lys Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr
      290     295     300
Tyr Val Tyr Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val
305     310     315     320
Val Glu Gly Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu
      325     330     335
Glu Val Lys Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr

```

403

```

          340          345          350
Leu Tyr Ser Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu
          355          360          365
Asp Asn Tyr Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile
          370          375          380
Ala Ile Val Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile
          385          390          395          400
Gln Lys Ala Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu
          405          410          415
Arg Ile Leu Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro
          420          425          430
Lys Pro Val Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr
          435          440          445
Ser Pro Glu Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Leu
          450          455          460
Ser Lys Arg Arg Phe Ile Leu
          465          470

```

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

```

Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly
1          5          10          15
Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
          20          25          30
Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
          35          40          45
Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
          50          55          60
Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
          65          70          75          80
Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
          85          90          95
Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
          100          105          110
Phe Gly Gly Val His Cys Gly His Gly Asp Phe
          115          120

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

404

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```

Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1           5           10           15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
          20           25           30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
          35           40           45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
          50           55           60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
65           70           75           80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
          85           90           95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
          100          105          110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```

Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1           5           10           15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
          20           25           30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
          35           40           45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
          50           55           60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
65           70           75           80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
          85           90           95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
          100          105          110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala

```

405

115

120

125

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

```

Met Ile Leu Ala Leu Leu Ile Ser Lys Glu Lys Thr His Leu Glu Ala
1      5      10      15
Leu Tyr Tyr Leu Ser Tyr Gly Val Leu Leu Gly Gly Val Ala Gln Ile
20     25     30
Leu Leu His Phe Tyr Pro Leu Val Lys Leu Gly Leu Trp Asp Leu Leu
35     40     45
Phe Lys Gly Leu Leu Gly Phe Lys Thr Lys Asn Thr Asn Lys Lys Glu
50     55     60
Tyr Arg Leu Asn Arg Ala Lys Lys Asp Leu Lys Ala Phe Phe Lys Gln
65     70     75     80
Phe Phe Pro Ser Val Leu Gly Asn Ser Ser Ala Gln Ile Ala Ser Phe
85     90     95
Leu Asp Thr Thr Ile Ala Ser Phe Leu Ala Ser Gly Ser Val Ser Tyr
100    105    110
Leu Tyr Tyr Ala Asn Arg Val Phe Gln Leu Pro Leu Ala Leu Phe Ala
115    120    125
Ile Ala Ile Ser Thr Ala Leu Phe Pro Ser Ile Ala Ile Ala Leu Lys
130    135    140
Asn Asn Gln Gln Asp Leu Ile Leu Gln Arg Leu Gln Lys Ala Trp Phe
145    150    155    160
Phe Leu Val Gly Val Leu Leu Leu Cys Ser Ile Gly Gly Ile Met Leu
165    170    175
Ser Lys Glu Ile Thr Glu Leu Leu Phe Glu Arg Gly Gln Phe Ser Pro
180    185    190
Lys Asp Thr Leu Ile Thr Ser Gln Val Phe Ser Leu Tyr Leu Leu Gly
195    200    205
Leu Leu Pro Phe Gly Leu Thr Lys Leu Phe Ser Leu Trp Leu Tyr Ala
210    215    220
Lys Leu Glu Gln Lys Lys Ala Ala Lys Ile Ser Leu Ile Ser Leu Phe
225    230    235    240
Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
245    250    255
Gly Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

406

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

Val Leu Lys Tyr Pro Thr Met Phe Met Cys Ala Asp Ala Val Ile Ile
 1 5 10 15
 Ser Lys Ala Asp Met Ile Glu Val Phe Asn Phe Arg Val Ser Gln Val

407

```

          20          25          30
Lys Glu Asp Met Gln Lys Leu Lys Pro Glu Ala Pro Ile Phe Leu Met
          35          40          45
Ser Ser Lys Asp Pro Lys Ser Leu Glu Asp Phe Lys Asn Phe Leu Leu
          50          55          60
Glu Lys Lys Arg Glu Asn Tyr Gln Ser Thr His Ser Phe
          65          70          75

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

```

Met Leu Leu Cys Ala Gly Arg Asn Glu Thr Leu Lys Lys Ala Val Pro
1          5          10          15
Ile Gly Val Gly Leu Ile Glu Ser Ala Ile Asn Leu Thr Arg Met Cys
          20          25          30
Leu Lys Asn Pro Asp Thr Glu Ser Leu Ile Phe Ile Gly Ser Ala Gly
          35          40          45
Ser Tyr Ser Pro Glu Thr Glu Ile Leu Ser Val Phe Glu Ser Ile Glu
          50          55          60
Gly Tyr Gln Ile Glu Glu Ser Phe Ser His Leu Asn Ser Tyr Thr Pro
          65          70          75          80
Leu Asp Asn Phe Ile His Ile Glu Thr Lys Glu Gln Ala Leu Phe Glu
          85          90          95
Arg Val Arg Val Asn Ser Ser Asn Tyr Ile His Thr Ser Glu Met Phe
          100          105          110
Ala Lys Lys Met Val Gln Lys Gly Val Leu Leu Glu Asn Met Glu Phe
          115          120          125
Phe Ser Val Leu Ser Val Ala Lys Ile Phe Ser Leu Lys Ala Lys Gly
          130          135          140
Ile Phe Cys Val Ser Asn His Val Gly Leu Asn Ala His Lys Glu Phe
          145          150          155          160
Lys Glu Asn His Ala Lys Val Lys Gln Ile Leu Glu Asn Ile Ile Asp
          165          170          175
Ser Leu Ile Val
          180

```

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

408

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

```

Val Tyr Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr
1      5      10      15
Ser Lys Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr
20     25     30
Asp Phe Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu
35     40     45
Ser Arg Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His
50     55     60
Ile Ala Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro
65     70     75     80
Ser Ala Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro
85     90     95
Thr Gln Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Ala Val Pro Lys
100    105    110
Leu Thr Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile
115    120    125
Gly Glu Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln
130    135    140
Leu Arg Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val
145    150    155    160
Asn Ile Leu Ala Pro Ile Val Gly Unk Lys Asn Unk Val Val Unk Unk
165    170    175
Val Asn Unk Glu Phe Unk Phe Unk Gln Lys Lys Ser Thr Lys Glu Thr
180    185    190
Phe Asp Pro Asn Asn Val Gly Lys Glu Arg Ala Lys Phe Arg Arg Lys
195    200    205
Lys Arg Arg Arg Ser
210

```

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

```

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg
1      5      10      15
Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala
20     25     30
Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe

```


409

```

      35              40              45
Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp
  50              55              60
Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp
  65              70              75              80
Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys
      85              90              95
Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met
      100              105              110
Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu
      115              120              125
Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met
      130              135              140
His Ile Arg Phe
145

```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp Ile
  1              5              10              15
Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys Ala Ile Gly
      20              25              30
Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr Ser Leu Met
      35              40              45
Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu Gln Ala Gln
      50              55              60
Ser Asn Asp Val Glu Ala Phe Pro Tyr Leu Ile Val Val Ile Asp Glu
      65              70              75              80
Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu Phe Pro Ile
      85              90              95
Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile Val
      100              105              110
Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys Thr
      115              120              125
Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp Ser
      130              135              140
Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg Gly
      145              150              155              160
Asp Met Leu Phe Thr Pro Pro Gly Thr Asn Gly Leu Val Arg Leu His
      165              170              175
Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe Ile
      180              185              190
Lys Ala Gln Lys Glu Val Glu Tyr Asp Lys Asp Phe Leu Leu Glu Glu
      195              200              205
Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu
      210              215              220

```

SUBSTITUTE SHEET (RULE 26)

410

```

Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser
225                230                235                240
Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
                245                250                255
Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
                260                265                270
Gly Asn Arg Glu Ile Leu Gln Asn Phe
                275                280

```

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

```

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser
1          5          10          15
His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly
          20          25          30
Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys
          35          40          45
Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala
          50          55          60
Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro
65          70          75          80
Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly
          85          90          95
Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser
          100         105         110
Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu
          115         120         125
Trp Cys Val Ser Glu Cys Gly Gly Gly Glu His Gln Arg Leu Lys Arg
          130         135         140

```

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

411

(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

```

Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
 1           5           10           15
Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Unk Tyr Thr
          20           25           30
Val Leu Leu Ser Pro Leu Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
          35           40           45
Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
          50           55           60
Pro Ser Val Glu Asn Val Gly Pro Ser
65           70

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

```

Val Cys Trp Thr Asp Leu Ile Gln Gly Leu Leu Met Met Ser Ala Leu
 1           5           10           15
Ile Val Val Pro Ile Val Met Ile Ile His Leu Gly Gly Ile Gly Glu
          20           25           30
Gly Ile Lys Ile Ile Arg Glu Ile Lys Pro Glu Asn Leu Ser Phe Unk
          35           40           45
Gln Gly Ser Ser Val Val Ala Ile Ile Ser Ser Leu Ala Trp Gly Leu
          50           55           60
Gly Tyr Phe Gly Gln Pro His Ile Leu Val Arg Phe Met Ser Ile Arg
          65           70           75           80
Ser Ile Arg Asp Val Pro Lys Ala Thr Thr Ile Gly Ile Ser Trp Met
          85           90           95
Val Ile Ser Leu Ile Gly Ala Cys Val Met Gly Leu Leu Gly Val Ala
          100          105          110
Tyr Val His Lys Unk Asp Leu Ser Leu Glu Asp Pro Glu Lys Ile Phe
          115          120          125
Ile Val Met Ser Gln Leu Leu Phe Asn Pro Trp Ile Thr Gly Ile Leu
          130          135          140
Leu Ser Ala Ile Leu Ala Ala Val Met Ser Thr Ala Ser Ser Gln Leu
          145          150          155          160
Leu Val Ser Ser Ser Thr Ile Ala Glu Asp Phe Tyr Ala Thr Ile Phe
          165          170          175
Asn Lys Asn Ala Pro Gln Lys Leu Val Met Thr Ile Ser Arg Leu Ser
          180          185          190
Val Leu Gly Val Ala Cys Ile Ala Phe Phe Ile Ser Thr Asp Lys Asn
          195          200          205
Ala Ser Ile Leu Ser Ile Val Ser Tyr Ala Trp Ala Gly Phe Gly Ala
          210          215          220

```

SUBSTITUTE SHEET (RULE 26)

412

```

Ser Phe Gly Ser Val Ile Leu Phe Ser Leu Phe Trp Ser Arg Met Thr
225                230                235                240
Arg Ile Gly Ala Ile Ala Gly Met Leu Ser Gly Ala Ser Thr Val Ile
                245                250                255
Leu Tyr Asp Lys Phe Gly Lys Ser Phe Leu Asp Ile Tyr Glu Ile Val
                260                265                270
Pro Gly Phe Ile Val Ala Ser Val Ala Ile Val Ala Phe Ser Leu Phe
                275                280                285
Ser Ser Val Arg Ser Gly Thr Lys Glu Ala Phe Glu Thr Met Leu Lys
                290                295                300
Glu Ile Glu Ser Leu Lys His
305                310

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

```

Val Gly Leu Phe Ile Val Leu Phe Leu Ile Ile Met Lys His Gln Thr
1          5          10          15
Ser Pro Tyr Ala Phe Thr His Asn Gln Ala Leu Val Thr Gln Thr Pro
          20          25          30
Pro Tyr Phe Thr Gln Leu Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser
          35          40          45
Ala His Ala Ser Ser Leu Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser
          50          55          60
Ala Tyr Phe Ser Gly Thr Lys Glu Gly Ala Arg Asp Val Lys Ile Ser
65          70          75          80
Ala Asn Leu Phe Asp Ser Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile
          85          90          95
Leu Leu Thr Lys Glu Leu Ser His His Ser His Glu Tyr Ile Lys
          100          105          110
Lys Ile Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

413

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

```

Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr Leu Ala Lys
1      5      10      15
Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr Lys Val Gly
20     25     30
Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu Gln Leu Ser
35     40     45
Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val Ile Asp Ala
50     55     60
Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys Asp Phe Ile
65     70     75     80
Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu Lys Ile Ala
85     90     95
Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp Val Ser Leu
100    105    110
Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp Ile Tyr Asp
115    120    125
Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr Lys Leu Asp
130    135    140
Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His Glu Ser Gln
145    150    155    160
Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro Met Asp Leu
165    170    175
Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu Asp Gly Phe
180    185    190
Ser Asn Pro Asn Lys Glu Gln Ala
195    200

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

```

Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly
1      5      10      15
Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu Gly Gly
20     25     30
Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met His Ser
35     40     45
Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys
50     55     60
Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala
65     70     75     80

```

414

```

Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg
      85          90          95
Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr
      100        105        110
Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly
      115        120        125
Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys Met Gln
      130        135        140
Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser Asn Glu
      145        150        155        160
Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr Phe Gly
      165        170        175
Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp Leu Leu
      180        185        190
Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu Asn Thr
      195        200        205
Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser Val Ile
      210        215        220
Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn Ala Gly
      225        230        235        240
Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly
      245        250        255
Asn Val Gly Met Arg Val Ala Phe
      260

```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

```

Met Asp Gly Tyr Gly Phe Lys Met Gln Asp Leu Gly Gln Lys Thr Gln
1      5      10      15
Val Ile Gln His Ile Phe Ala Gly Asp Asp Val Ser Ala Leu Glu Val
      20      25      30
Lys Glu Asn Glu Cys Val Lys Ile Met Thr Gly Ala Met Val Pro Lys
      35      40      45
Gly Ile Glu Thr Ile Val Pro Ile Glu Cys Met Leu Glu Ser His Lys
      50      55      60
Asp Phe Ala Leu Ala Pro Lys Asp Phe Lys Ile His Ala Asn Ile Arg
65      70      75      80
Gln Lys Gly Glu Asn Ala Ser Leu Asn Ser Val Leu Val Pro Lys Asn
      85      90      95
Thr Arg Leu Asn Tyr Gly His Ile Ala Leu Ile Ala Ser Gln Gly Phe
      100     105     110
Lys Glu Ile Lys Ala Phe Arg Lys Leu Lys Ile Ala Leu Phe Ser Ser
      115     120     125
Gly Asp Glu Leu Val Pro Leu Gly Gln Asn Ala Leu Glu Cys Gln Val
      130     135     140
Tyr Asp Val Asn Ser Val Gly Val Phe Asn Met Leu Lys Asn Tyr Asn

```

415

```

145          150          155          160
Thr His Phe Leu Gly Val Leu Lys Asp Asp Lys Asn Leu Gln Leu Lys
          165          170          175
Ile Leu Glu Leu Gln Gly Tyr Asp Val Ile Leu Ser Ser Ala Gly Val
          180          185          190
Ser Val Gly Asp Lys Asp Phe Phe Lys Asp Ala Leu Lys Glu Arg Asn
          195          200          205
Ala Leu Phe Tyr Tyr Glu Lys Val Asn Leu Lys Pro Gly Lys Pro Val
          210          215          220
Thr Leu Ala Gln Leu Asn Gln Ser Ile Ile Ile Gly Leu Pro Gly Asn
225          230          235          240
Pro Leu Ser Cys Leu Leu Val Leu Arg Val Leu Ile Leu Pro Leu Leu
          245          250          255
Glu Arg Leu Ser Leu Asn Lys Asp Phe Lys Leu Lys Pro Phe Lys Ala
          260          265          270
Gln Ile Asn Ala Pro Leu Lys Leu Asn Asn Lys Arg Thr His Leu Ile
          275          280          285
Leu Gly Asn Tyr Ser Asn His Gln Phe Ile Pro Tyr Asn Asn Arg Tyr
          290          295          300
Glu Ser Gly Ala Ile Gln Ala Leu Ala Gln Val Asp Ser Ile Thr Leu
305          310          315          320
Ile Asp Glu Gly Val Gly Leu Val Gln Gly Glu Ile Glu Ile Leu Arg
          325          330          335
Phe Glu Asn

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

```

Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu Phe
1          5          10          15
Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu Phe
          20          25          30
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys
          35          40          45
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser
          50          55          60
Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys Thr
65          70          75          80
Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser
          85          90          95
Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Ile
          100          105          110
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met Asn
          115          120          125
Thr Leu Leu Ala Tyr Phe Glu His Gln Lys Gln Arg Phe Gln Tyr Pro
130          135          140

```

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Ser Leu
145

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

```

Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser
1      5      10      15
Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln
20      25      30
Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly
35      40      45
Leu Asp Gly Arg Val Ala Arg Leu Thr Lys His His
50      55      60

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

```

Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1      5      10      15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
20      25      30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
35      40      45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
50      55      60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
65      70      75      80
Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln

```


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				85					90					95			
Lys	Met	Phe	Glu	Ser	Tyr	Gly	Val	Asn	Pro	Phe	Lys	Asp	Leu	Ile	Glu		
			100					105					110				
Arg	Pro	Asn	Ile	Pro	Asn	Ile	Pro	Asn	Ile	Ala	Asn	Pro	Ile	Ala	Ile		
		115					120					125					
Ile	Asp	Gly	Ile	Ser	Phe	Ile	Lys	Ser	Met	Arg	Leu	Lys	His	Glu	Asn		
	130					135					140						
Leu	Lys	Asn	Asn	Gln	Thr	Ser	Leu	Gly	Glu	Val	Leu	Lys	Leu	Leu	Asp		
145				150						155					160		
Gln	Lys	His	Gln	Leu	Leu	Asn	Gln	Trp	His	Ala	Leu	Asp	Lys	Ser	Ala		
			165						170					175			
Lys	Leu	Ser	Asp	Glu	Ile	Tyr	Gln	Thr	Gln	Ala	Lys	Arg	Leu	Glu	Leu		
		180						185					190				
Gln	Gly	Ala	Gln	Asn	Ile	Leu	Lys	Thr	Thr	Ile	Gly	Ile	Phe	Gln	Lys		
	195					200					205						
Asp	Ser	Asp	Glu	Ala	Ile	Ser	Ile	Val	Lys	Ser	Gln	Val	Lys	Asn	Gln		
	210					215					220						
Leu	Phe	Lys	Leu	Val	Tyr	Val	Phe	Leu	Ala	Ala	Leu	Leu	Ser	Val	Val		
225				230						235					240		
Phe	Ala	Trp	Ile	Leu	Lys	Ile	Ile	Ser	Ser	Lys	Tyr	Ile	Glu	Asn	Asn		
			245						250					255			
Glu	Arg	Val	Tyr	Thr	Val	Asn	Lys	Ala	Ile	Asn	Phe	Val	Asn	Val	Ser		
		260						265					270				
Val	Ile	Unk	Unk	Ile	Unk	Leu	Phe	Ser	Tyr	Leu	Glu	Asn	Val	Thr	Tyr		
	275					280					285						
Leu	Val	Thr	Val	Leu	Gly	Phe	Ala	Ser	Ala	Gly	Leu	Ala	Ile	Unk	Met		
	290				295					300							
Lys	Asp	Leu	Phe	Met	Ser	Leu	Leu	Gly	Trp	Phe	Ile	Ile	Leu	Ile	Gly		
305				310						315					320		
Gly	Ser	Val	His	Val	Gly	Asp	Arg	Val	Arg	Ile	Ala	Lys	Gly	Thr	Asp		
			325						330					335			
Ile	Phe	Ile	Gly	Asp	Val	Leu	Asp	Thr	Ser	Asn	Val	Val	His				
	340							345					350				

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala
1				5					10					15	
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Ser	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu
			20					25					30		
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe	
		35					40					45			
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val
		50				55					60				
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu
65				70						75				80	

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```

Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln
      85                      90                      95
Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu
      100                    105                    110
Arg Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile
      115                    120                    125
Ile Asp Gly Ile Ser Phe Ile Lys Ser Met Arg Leu Lys His Glu Asn
      130                    135                    140
Leu Lys Asn Asn Gln Thr Ser Leu Gly Glu Val Leu Lys Leu Leu Asp
      145                    150                    155                    160
Gln Lys His Gln Leu Leu Asn Gln Trp His Ala Leu Asp Lys Ser Ala
      165                    170                    175
Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu
      180                    185                    190
Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys
      195                    200                    205
Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln
      210                    215                    220
Leu Phe Lys Leu Val Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val
      225                    230                    235                    240
Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn
      245                    250                    255
Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser
      260                    265                    270
Val Ile Unk Ile Unk Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr
      275                    280                    285
Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Unk Met
      290                    295                    300
Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly
      305                    310                    315                    320
Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp
      325                    330                    335
Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His
      340                    345                    350

```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

```

Met Leu Ser Ala Leu Leu Ser Lys Met Gly Thr Tyr Ala Leu Leu Arg
1      5      10      15
Phe Leu Leu Pro Leu Phe Pro Glu Leu Ser Glu Ile Tyr Leu Thr Pro
      20      25      30
Ile Ala Ile Val Ala Leu Cys Met Ile Ile Tyr Gly Gly Phe Leu Ala
      35      40      45
Tyr Ala Gln Lys Asp Leu Lys Thr Leu Ile Ala Tyr Ser Ser Phe Ser
      50      55      60
His Met Gly Val Val Val Leu Gly Val Phe Ser Phe Asn Val Glu Gly

```

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```

65          70          75          80
Val Ser Gly Ala Val Phe Met Met Phe Ala His Gly Val Ile Val Met
      85          90
Gly Leu Phe Leu Leu Ala Gly Ile Leu Glu Glu Arg Ala Ser Ser Leu
      100          105          110
Glu Ile Ala Arg Phe Gly Ser Ile Ala Lys Ser Ala Pro Val Phe Ala
      115          120          125
Ala Phe Phe Met Ile Val Leu Met Ala Asn Val Gly Met Pro Leu Ser
      130          135          140
Ile Gly Phe Val Gly Glu Phe Leu Asn Leu Leu Gly Phe Phe Ala Thr
145          150          155          160
Tyr Pro Leu Leu Ala Ile Ile Ala Gly Thr Ser Leu Ile Leu Ser Ala
      165          170          175
Val Tyr Ile Leu Thr Ser Tyr Lys Asp Val Phe Phe Gly Asn Leu Lys
      180          185          190
Thr Gly Asn Asn Gln Ile Ser Val Phe Glu Asp Leu Asn Ala Arg Glu
      195          200          205
Val Gly Val Leu Ser Val Ile Leu Ala Phe Asp Leu Asn Phe Arg Asp
210          215          220
Leu Tyr Lys Ser Ala Phe Lys Thr Asp
225          230

```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

```

Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val
1          5          10          15
Ile Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
      20          25          30

```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

420

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

```

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys
1      5      10      15
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr
      20      25      30
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr
      35      40      45
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr
      50      55      60
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala
      65      70      75      80
Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
      85      90      95
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
      100     105     110
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Arg Ala Ile Glu Glu
      115     120     125
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
      130     135     140
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Pro Leu Tyr
      145     150     155     160
Arg Ala Phe Glu Ala Leu Tyr Thr Gln Thr Phe
      165     170

```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

```

Val Arg Ala Val Phe Val Phe Gly Leu Lys Ala Ala Phe Cys Ile Gly
1      5      10      15
Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe Leu Asp Glu Phe Leu Ile Lys
      20      25      30
Leu

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

421

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

```

Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1          5          10          15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
          20          25          30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
          35          40          45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
          50          55          60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65          70          75          80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
          85          90          95
Phe Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

```

Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1          5          10          15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
          20          25          30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
          35          40          45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
          50          55          60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65          70          75          80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
          85          90          95
Phe Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:508:

422

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1      5      10      15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
      20      25      30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
      35      40      45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
50      55      60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1      5      10      15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
      20      25      30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
      35      40      45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
50      55      60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:

423

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1          5          10          15
Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
20          25          30
Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
35          40          45
Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
50          55          60
Gln Pro Gly Gln Arg Ala
65          70

```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

```

Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly Ser
1          5          10          15
Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu Met
20          25          30
Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly Cys
35          40          45
Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe Gly
50          55          60
Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe Thr
65          70          75          80
Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys Ser
85          90          95
Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu Gly
100          105          110
Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val Gly
115          120          125

```

424

Val Asn
130

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

```

Leu Gly Leu Val Unk Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
1          5          10          15
Lys Ile Ser Val Phe Leu Gly Unk Asn Leu Met Leu Tyr Pro Val Unk
          20          25          30
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
          35          40          45
Thr His Ala Gly
50

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

```

Leu Gly Leu Val Unk Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
1          5          10          15
Lys Ile Ser Val Phe Leu Gly Unk Asn Leu Met Leu Tyr Pro Val Unk
          20          25          30
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
          35          40          45
Thr His Ala Gly
50

```

(2) INFORMATION FOR SEQ ID NO:512:

425

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...79
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```

Met Leu Glu Lys Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu
 1             5             10             15
Leu Ala Pro Leu Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly
             20             25             30
Tyr Val Phe Met Lys Glu Leu Trp His Met Leu Ser His Leu Asn Thr
             35             40             45
Ile Ser Glu Thr Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu
             50             55             60
Leu Val His Gly Arg Ala Cys Phe Asp Gly Ala Ala Arg Gln Leu
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

```

Met His Tyr Gln Leu Thr Ser Phe Asn Ile Ile Gln Asp Leu Phe Ile
 1             5             10             15
Thr Cys His Val Leu Arg Ile Lys Met Arg Val Phe Val Cys Phe Leu
             20             25             30
Gly Val Phe Val Ser Asn Gly Leu Ala Arg Phe Gly Tyr Val Val Leu
             35             40             45
Ile Pro Leu Leu Ile Leu Ser Gly Ser Leu Thr Pro His Gln Ser Phe
             50             55             60
Gln Leu Gly Ile Ala Val Leu Met Gly Tyr Val Phe Gly Ser Phe Leu
65             70             75             80
Ile Gln Phe Leu Ser Pro Leu Met Ser Leu Lys Ser Ile Ala Lys Ile
             85             90             95
Ser Phe Lys Leu Thr Leu
100

```

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(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

```

Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys Leu Unk Arg Ala
1           5           10          15

```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```

Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1           5           10          15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
20          25          30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
35          40          45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
50          55          60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
65          70          75          80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
85          90          95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
100         105         110
Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
115         120         125
Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
130         135         140
Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn

```

427

```

145          150          155          160
Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
      165          170          175
Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
      180          185          190
Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
      195          200          205
Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
      210          215          220
Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
225          230          235          240
Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
      245          250          255
Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
      260          265          270
Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
      275          280          285
Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
290          295          300
Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
305          310          315          320
Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
      325          330          335
Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
      340          345          350
Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
      355          360          365
His Ser Ile Ile Asp Lys Tyr Gln Pro
370          375

```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```

Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1          5          10          15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
      20          25          30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
      35          40          45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
50          55          60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
65          70          75          80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
      85          90          95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
100          105          110

```

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Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
 115 120 125
 Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
 130 135 140
 Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn
 145 150 155 160
 Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
 165 170 175
 Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
 180 185 190
 Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
 195 200 205
 Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
 210 215 220
 Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
 225 230 235 240
 Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
 245 250 255
 Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
 260 265 270
 Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
 275 280 285
 Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
 290 295 300
 Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
 305 310 315 320
 Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
 325 330 335
 Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
 340 345 350
 Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
 355 360 365
 His Ser Ile Ile Asp Lys Tyr Gln Pro
 370 375

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1027 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Val Cys Leu Asp His Gln Val Gly Ala Gly Lys Thr Leu Cys Ala Ile
 1 5 10 15
 Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu Val Asn Lys Thr Leu
 20 25 30
 Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp Gly Asp Glu Phe Tyr
 35 40 45
 Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val Asp Ser Lys Asp Thr
 50 55 60
 Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln Ile Ala Asn Asn Asn

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65		70		75		80									
Tyr	Asp	Ala	Val	Val	Ile	Ala	His	Thr	His	Leu	Glu	Leu	Leu	Ser	Asn
			85						90					95	
Pro	Arg	Gly	Ile	Ile	Glu	Glu	Leu	Lys	Glu	Glu	Glu	Leu	Val	Asn	Ala
			100						105					110	
Glu	Lys	Asn	Phe	Glu	Arg	Gln	Glu	Leu	Ala	Tyr	Lys	Asn	Asn	Pro	Arg
			115						120					125	
Glu	Thr	Lys	Lys	Pro	Asn	Glu	Arg	Ala	Phe	Lys	Asn	Lys	Leu	Asp	Lys
			130						135					140	
Ile	Arg	Ala	Lys	Tyr	Asp	Ala	Ile	Leu	Glu	Lys	Gln	Gly	Ser	His	Ile
			145						150					155	
Asp	Ile	Ser	Gln	Met	Gly	Ile	Asp	Asn	Leu	Ile	Val	Asp	Glu	Ala	His
			165						170					175	
Leu	Phe	Lys	Asn	Leu	Ala	Phe	Glu	Thr	Ser	Met	Glu	Lys	Ile	Ala	Gly
			180						185					190	
Leu	Gly	Asn	Gln	Gln	Gly	Ser	Asn	Arg	Ala	Arg	Asp	Leu	Phe	Ile	Lys
			195						200					205	
Thr	Arg	Tyr	Leu	His	Gln	Asn	Asp	Lys	Lys	Ile	Met	Phe	Leu	Thr	Gly
			210						215					220	
Thr	Pro	Ile	Ala	Asn	Ser	Leu	Ser	Glu	Met	Tyr	His	Leu	Gln	Arg	Tyr
			225						230					235	
Leu	Thr	Pro	Asp	Val	Leu	Lys	Glu	Arg	Gly	Leu	Glu	Phe	Phe	Asp	Asp
			245						250					255	
Trp	Ala	Lys	Thr	Tyr	Gly	Glu	Val	Val	Asn	Asp	Phe	Glu	Leu	Asp	Thr
			260						265					270	
Ser	Ala	Gln	Ser	Tyr	Lys	Met	Val	Asn	Arg	Phe	Ser	Lys	Phe	Ser	Asp
			275						280					285	
Val	Gln	Gly	Leu	Ser	Thr	Met	Tyr	Arg	Ala	Phe	Ala	Asp	Ile	Val	Ser
			290						295					300	
Asn	Asp	Asp	Ile	Leu	Lys	His	Asn	Pro	His	Phe	Val	Pro	Lys	Val	Tyr
			305						310					315	
Gly	Asp	Lys	Pro	Ile	Asn	Val	Val	Val	Lys	Arg	Ser	Glu	Glu	Val	Ala
			325						330					335	
Gln	Phe	Ile	Gly	Val	Ala	Leu	Glu	Asn	Gly	Lys	Tyr	Asn	Glu	Gly	Ser
			340						345					350	
Ile	Ile	Asp	Arg	Met	Gln	Lys	Cys	Glu	Gly	Lys	Lys	Ser	Gln	Lys	Gly
			355						360					365	
Gln	Asp	Asn	Ile	Leu	Ser	Cys	Thr	Thr	Asp	Ala	Arg	Lys	Val	Ala	Leu
			370						375					380	
Asp	Tyr	Arg	Leu	Ile	Asp	Pro	Asn	Ala	Lys	Val	Glu	Lys	Glu	Phe	Ser
			385						390					395	
Lys	Ser	Tyr	Ala	Met	Ala	Lys	Asn	Ile	Tyr	Glu	Asn	Tyr	Leu	Glu	Thr
			405						410					415	
His	Ala	Thr	Lys	Gly	Thr	Gln	Leu	Gly	Phe	Ile	Gly	Leu	Ser	Thr	Pro
			420						425					430	
Lys	Thr	His	Ser	Gln	Lys	Val	Ser	Leu	Glu	Ala	Leu	Asp	Asn	Ala	His
			435						440					445	
Glu	Thr	Glu	Asn	Lys	Asn	Pro	Leu	Asp	Lys	Ala	Gln	Glu	Leu	Leu	Glu
			450						455					460	
Ser	Leu	Ser	Ser	Tyr	Asp	Glu	Lys	Gly	Asn	Leu	Ile	Ala	Pro	Ser	Lys
			465						470					475	
Lys	Glu	Leu	Glu	Asn	Glu	Leu	Lys	Glu	Lys	Glu	Ala	Lys	Ser	Val	Asn
			485						490					495	
Leu	Asp	Glu	Glu	Ile	Ala	Lys	Gly	Cys	Ser	Phe	Asp	Val	Tyr	Ser	Asp
			500						505					510	
Val	Leu	Arg	His	Leu	Val	Gln	Met	Gly	Ile	Pro	Gln	Asn	Glu	Ile	Ala
			515						520					525	
Phe	Ile	His	Asp	Ala	Lys	Thr	Glu	Glu	Gln	Lys	Gln	Asp	Leu	Phe	Lys
			530						535					540	
Lys	Leu	Asn	Arg	Gly	Gly	Val	Arg	Val	Leu	Leu	Gly	Ser	Pro	Ala	Lys
			545						550					555	
Met	Gly	Val	Gly	Thr	Asn	Val	Gln	Glu	Arg	Leu	Val	Ala	Met	His	Glu
			565						570					575	
Leu	Asp	Cys	Pro	Trp	Arg	Pro	Asp	Glu	Leu	Leu	Gln	Met	Glu	Gly	Arg
			580						585					590	

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Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn Asp Pro Glu Asn Phe
 595 600 605
 Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys Thr Tyr Asp Ser Arg
 610 615 620
 Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly Ile Glu Gln Phe Arg
 625 630 635 640
 Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu Asp Phe Asn Met Gly
 645 650 655
 Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala Thr Gly Asn Pro Leu
 660 665 670
 Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile Lys Ser Glu Glu Ser
 675 680 685
 Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe Asn Glu Glu Ser Leu
 690 695 700
 Lys Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys Gln Glu Leu Lys Asp
 705 710 715 720
 Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro Thr His Thr Glu Ile
 725 730 735
 Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys Asp Tyr Glu Leu Ile
 740 745 750
 Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn Ala Ser Met Ser Glu
 755 760 765
 Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn Lys Gln Ile Ala Glu
 770 775 780
 Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys Gln Phe Ala Ser Asn
 785 790 795 800
 Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp Tyr Lys Leu Leu Glu
 805 810 815
 Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr Lys Tyr Gln Val Glu
 820 825 830
 Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile Ala Tyr Ser Pro Ser
 835 840 845
 Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met Phe Ser Ser Tyr Asn
 850 855 860
 Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu Lys Arg Leu Asp Asn
 865 870 875 880
 Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu Leu Glu Asn Ser Ile
 885 890 895
 Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr Arg Leu Val Glu Gln
 900 905 910
 Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln Ala Leu Lys Trp Asp
 915 920 925
 His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met Ser Lys Asp Arg Asn
 930 935 940
 Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu Val Leu Lys Asn Leu
 945 950 955 960
 Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu Arg Glu Glu Gln Gly
 965 970 975
 Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile Glu Pro Ala Thr Glu
 980 985 990
 Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp Glu Ile Ala Asn Asn
 995 1000 1005
 Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu Ile Thr Lys Ser Met
 1010 1015 1020
 Gly Arg Arg
 1025

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

```

Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1      5      10      15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
20     25     30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
35     40     45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
50     55     60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65     70     75     80
Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
85     90     95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
100    105    110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
115    120    125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
130    135    140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145    150

```

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

```

Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1      5      10      15
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
20     25     30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
35     40     45
Ala Tyr Gly Ile Ser Asp Val Unk Unk Ser Lys Ala Lys Lys Asp Lys
50     55     60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65     70     75     80

```

432

```

Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
      85                      90                      95
Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
      100                    105                    110
Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
      115                    120                    125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
      130                    135                    140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145                      150

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

```

Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala Lys Lys Ile Gln
1      5                      10                      15
Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met Glu Val Val Gly
      20                    25                    30
Val Phe Arg Val Ile Gly Trp Ala Asn Glu Tyr Phe Cys Phe Phe Tyr
      35                    40                    45
Met Val Gly Gly Met Ala Leu Ala Arg Cys Ile Ala Met Cys
50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

```

Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe Leu Leu Leu Ser
1      5                      10                      15
Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys Gln Leu Asp Asn

```


433

```

      20      25      30
Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn Leu Asp Glu Ile
      35      40      45
Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile Gly Gln Glu Asp
      50      55      60
Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg Gly Asp Leu Ala
      65      70      75      80
Leu Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe Phe Ile Ser Glu
      85      90      95
Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu Leu Leu Thr
      100      105      110
Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala Glu Gln Gln Cys
      115      120      125
Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu Gly Lys Leu Lys
      130      135      140
Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu Glu Thr Ser Leu
      145      150      155      160
Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser Leu Ile Thr Ala
      165      170      175
Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn Phe Ile Lys Gly
      180      185      190
Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe Leu Asn Tyr Leu
      195      200      205
Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln Ser Lys Arg Gln
      210      215      220
Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val Lys
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

```

Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1      5      10      15
Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
      20      25      30
Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
      35      40      45
Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
      50      55      60
Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
      65      70      75      80
His Asn Asp

```

(2) INFORMATION FOR SEQ ID NO:521:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

435

```

Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys Ala
1          5          10          15
Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Gly Glu
          20          25          30
Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn Glu
          35          40          45
Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro Ser
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

```

Met Leu Val Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys
1          5          10          15
Ala Leu Asp Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly
          20          25          30
Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu
          35          40          45
Ala Gly Leu Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln
          50          55          60
Lys Ile Gly Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly
65          70          75          80
Asp Phe Leu Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr
          85          90          95
Lys Asp Phe Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu
          100          105          110
Lys Arg Phe Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys
          115          120          125
Gly Met Arg Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala
          130          135          140
Ser Leu Tyr Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala
145          150          155          160
Arg Glu Glu Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala
          165          170          175
Ser Leu Leu Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu
          180          185          190
Asp Ser Ala Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp
          195          200          205
Val Gly Glu Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys
210          215          220
Glu Arg Leu Lys
225

```

(2) INFORMATION FOR SEQ ID NO:524:

436

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

```

Met Asn Lys Leu Phe Leu Ala Phe Ile Val Gly Gly Met Leu Leu Ser
1      5      10      15
Ala Asp Ala Leu Asn Asp Lys Ile Glu Asn Leu Met Gly Glu Arg Ser
20     25     30
Tyr His Met Asn Lys Leu Phe Leu Glu Arg Leu Phe Lys Asn Arg Lys
35     40     45
Asp Phe Tyr Glu Met Gly Arg Leu Asp Ser Leu Lys Leu Leu Asn Thr
50     55     60
Leu Lys Glu Asn Gly Leu Leu Ser Phe Asn Phe Asp Lys Pro Ser Val
65     70     75     80
Leu Lys Ile Thr Phe Lys Ala Ser Ser Asn Pro Leu Ala Phe Ala Lys
85     90     95
Ser Ile Asn Asn Ser Leu Asn Met Met Gly Tyr Ser Tyr Val Leu Pro
100    105    110
Ile Arg Met Gln Ser Ser Ser Gly Glu Asn Val Phe Ser Tyr Glu Leu
115    120    125
Lys Thr Glu Tyr Val Leu Asp Pro Asn Ile Leu Ile Glu Thr Met Lys
130    135    140
Arg His Gly Phe Asp Phe Met Asp Ile Arg Arg Val Ser Leu Lys Glu
145    150    155    160
Trp Glu Tyr Asp Phe Ala Leu Gln Lys Ile Lys Leu Pro Asn Ala Arg
165    170    175
Ala Leu Val Leu Ser Ser Asp Pro Val Glu Phe Lys Glu Ala Ser Gly
180    185    190
Lys Tyr Trp Leu Ser Val Asn Gln Asn Ala Tyr Leu Lys Ile Ser Ser
195    200    205
Asn Asn Pro Leu Trp Gln Pro Lys Ile Ile Phe Tyr Asp Glu Asn Leu
210    215    220
Lys Ile Ile Gln Ile Ile Ala Lys Glu Asn Arg Gln Gln Glu Ile Ala
225    230    235    240
Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp Ala Lys
245    250    255
Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp Ala Met
260    265    270
Pro

```

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

437

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

Val	Ser	Arg	Pro	Phe	Lys	Thr	Ile	Lys	Lys	Pro	Pro	Gln	Pro	Pro
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

Met	Unk	Thr	His	Asp	Arg	Arg	Lys	Leu	Arg	Ile	Unk	Leu	Thr	Gln	Thr
1				5				10					15		
Thr	Thr	Leu	Val	Ala	Thr	Ile	Gly	Ser	Asn	Ala	Pro	Tyr	Ile	Gly	Leu
		20					25					30			
Leu	Gly	Thr	Val	Met	Gly	Ile	Met	Leu	Thr	Phe	Met	Asp	Leu	Gly	Ser
		35				40					45				
Ala	Ser	Gly	Ile	Asp	Thr	Lys	Ala	Ile	Met	Thr	Asn	Leu	Ala	Leu	Ala
		50				55				60					
Leu	Lys	Ala	Thr	Gly	Met	Gly	Leu	Leu	Val	Ala	Ile	Pro	Ala	Ile	Val
65				70				75						80	
Ile	Tyr	Asn	Leu	Leu	Val	Arg	Lys	Ser	Glu	Ile	Leu	Val	Thr	Lys	Trp
		85				90							95		
Asp	Ile	Phe	His	Pro	Val	Asp	Thr	Gln	Ser	His	Glu	Val	Tyr	Ser	
		100				105						110			
Lys	Ala														

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

```

Met Unk Thr His Asp Arg Arg Lys Leu Arg Ile Unk Leu Thr Gln Thr
1          5          10          15
Thr Thr Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu
20          25          30
Leu Gly Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser
35          40          45
Ala Ser Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala
50          55          60
Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
65          70          75          80
Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
85          90          95
Asp Ile Phe His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
100          105          110
Lys Ala

```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

```

Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
1          5          10          15
Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
20          25          30
Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
35          40          45
Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
50          55          60
Tyr Pro Asn
65

```

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

439

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```

Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile Ala
1      5      10      15
Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala Arg
20      25      30
Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe Ala
35      40      45
Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu Leu
50      55      60
Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr Ser
65      70      75      80
Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu Asn
85      90      95
Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu Ala
100     105     110
Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr Val
115     120     125
Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu Lys
130     135     140
Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu Glu
145     150     155     160
Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr Ile
165     170     175
Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp Ala
180     185     190
Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys Ile
195     200     205
Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln Glu
210     215     220
Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp Asp
225     230     235     240
Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln Asp
245     250     255
Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln Ile
260     265     270
Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys Ala
275     280     285
Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe Pro
290     295     300
Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met Asp
305     310     315     320
Met Val Ala

```

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

Met	Glu	His	Leu	Thr	Arg	Gly	Ile	Lys	His
1				5				10	

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

Val	Val	Ile	Leu	Gly	Ser	His	Gly	Lys	Glu	Glu	Tyr
1				5					10		

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Met	Lys	Lys	Val	Ile	Val	Ala	Leu	Gly	Val	Leu	Ala	Phe	Ala	Asn	Val
1				5				10				15			
Leu	Met	Ala	Thr	Asp	Val	Lys	Ala	Leu	Val	Lys	Gly	Cys	Ala	Ala	Cys
				20				25				30			
His	Gly	Val	Lys	Phe	Glu	Lys	Lys	Ala	Leu	Gly	Lys	Ser	Lys	Ile	Val

441

```

      35          40          45
Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp Leu Met Ala Phe Lys
  50          55          60
Ser Gly Ala Asn Lys Asn Pro Val Met Thr Arg Lys Leu Lys Asn
  65          70          75

```

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

```

Met Gly Ile Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr
 1          5          10          15
Ala Leu Lys Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys
 20          25          30
Tyr Ala Ser His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu
 35          40          45
Ala Ile Cys Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys
 50          55          60
Glu Gly Leu Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala
 65          70          75          80
Arg Leu Met His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro
      85          90          95

```

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533

```

Met His Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu
 1          5          10          15
Pro Lys Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala
 20          25          30

```

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```

Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
      35              40              45
Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
      50              55              60
His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
      65              70              75              80
Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
      85              90              95
Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
      100             105             110
Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
      115             120             125
Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
      130             135             140
Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
145              150

```

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1      5              10              15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
      20              25              30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
      35              40              45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
      50              55              60
Lys Gln Gln
65

```

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

443

(A) NAME/KEY: misc_feature
(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1          5          10          15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
20          25          30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
35          40          45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
50          55          60
Lys Gln Gln
65

```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

```

Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1          5          10          15
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
20          25          30
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys Lys Tyr
35          40          45
Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
50          55          60
Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65          70          75          80
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
85          90          95
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
100          105          110
Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile Met Leu
115          120          125
Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
130          135          140
Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys Glu Ile
145          150          155          160
Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu Lys Lys
165          170          175
Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu Thr Asn
180          185          190
Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp Glu Asn
195          200          205
His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr Pro Tyr
210          215          220

```

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```

Asn Thr Thr Leu Asn Asn Ser Glu Pro Gln Glu Gly Leu Val Gln Ile
225                230                235                240
Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
                245                250                255
Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
                260                265                270
Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
                275                280                285
Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
290                295                300
Lys Thr Thr Lys Pro Leu Thr Thr Pro
305                310

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

```

Val Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu
1          5          10          15
Leu Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His
          20          25          30
Leu Pro Glu Ile Thr Leu Asp Tyr Leu Asn Arg Gln Ile Ser Lys Met
          35          40          45
Gln Ala Glu Ile Lys Met Ala Lys Ser Phe Phe Val Leu Asp Ala Lys
          50          55          60
Gly Met Leu Met Leu Lys Pro Ser Gln Phe Lys Glu Gln Gly His Lys
65          70          75          80
Glu Gly Leu Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser
          85          90          95
His Val Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Asn Glu
          100         105         110
Lys Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His
          115         120         125
Leu Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu
          130         135         140
Ala Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile
145         150         155         160
Ser Ser Pro Ser Lys Tyr Phe Lys Thr Phe Ser Glu Gly Ser Met Val
          165         170         175
Met Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu
          180         185         190
Phe Val Lys Cys Ile Ser Ser Phe Trp Thr Ala Ile Val His Phe Ser
          195         200         205
Ser Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu
          210         215         220
Ala Leu Ala Thr Phe Asp Leu Val Lys Ala Ile Phe Glu Glu Glu Val
225         230         235         240
Leu Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met

```

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```

                245                250                255
Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu
                260                265                270
Met Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr
                275                280                285
Ala Val Tyr Leu Ala Ile Gly Val Ala Val Leu Leu Ile Ser Leu Ala
                290                295                300
Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg
305                310                315

```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537

```

Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser
1          5          10          15
Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe
          20          25          30
Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp
          35          40          45
Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser
50          55          60
Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe
65          70          75          80
Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu
          85          90          95
Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile
          100          105          110
Gly Gly Leu Ser Phe Leu
115

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

446

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

```

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1      5      10      15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
20      25      30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
35      40      45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
50      55      60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65      70      75      80
Phe Ile Phe Ser His Phe Phe Ser
85

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

```

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1      5      10      15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
20      25      30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
35      40      45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
50      55      60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65      70      75      80
Phe Ile Phe Ser His Phe Phe Ser
85

```

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

447

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539

```

Met Phe Lys Ser Arg Leu Asn Ser Trp Ile Leu Leu Gly Ile Leu Gly
1           5           10           15
Val Leu Val Val Val Phe Trp Asp Val Ile Lys Tyr Lys Ile Glu Asp
          20           25           30
Leu Gln His Asp His Tyr Leu Ser Gln Val Lys Glu Arg Glu Glu Tyr
          35           40           45
Tyr Lys Asn His Ile Glu Glu Ala Leu Lys Lys Asp Ser Glu Cys Phe
50           55           60
Glu Lys Gly Gly Asp Lys Val Asp Cys Ser Ala Ala Met Arg Ile Ala
65           70           75           80
Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys
          85           90

```

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540

```

Met Val Phe Trp Gly Ala Val Phe Phe Leu Trp Asp Arg Thr Ala Trp
1           5           10           15
Lys Arg Leu Met Val Phe Leu Asn Ser Leu Unk Unk Met Leu Ala Ala
          20           25           30
Leu Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His
          35           40           45
Thr Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met
50           55           60
Gly Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe
65           70           75           80
Val Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu
          85           90           95
Asn Gln Met His Ala Glu Phe Ile Asp Val Ser Ile His Phe Tyr Ala
          100          105          110
Leu Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu
          115          120          125
Ser Ser Leu Lys Lys Ala Cys Glu Asn Ala
          130          135

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

```

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1      5      10      15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
      20      25      30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
      35      40      45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
      50      55      60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65      70      75      80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
      85      90      95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
      100     105     110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
      115     120     125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
      130     135     140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145     150     155     160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
      165     170     175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
      180     185     190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
      195     200     205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
      210     215     220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225     230     235     240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
      245     250     255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
      260     265     270
Lys Lys Ser Pro
      275

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

449

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

```

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1      5      10      15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
      20      25      30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
      35      40      45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
      50      55      60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
      65      70      75      80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
      85      90      95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
      100      105      110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
      115      120      125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
      130      135      140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
      145      150      155      160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
      165      170      175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
      180      185      190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
      195      200      205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
      210      215      220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
      225      230      235      240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
      245      250      255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
      260      265      270
Lys Lys Ser Pro
      275

```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...254

450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542

```

Met His Glu Gln Gly Ser Ile Ser Phe Ile Gly Glu Gln Gly Ala Lys
1      5      10      15
Arg Leu Leu Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn
20      25      30
Lys Ile Ala Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val
35      40      45
Ala Arg Thr Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe
50      55      60
Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys
65      70      75      80
Asp Tyr Arg Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr
85      90      95
Val Met Tyr Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg
100     105     110
Tyr Gly Phe Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys
115     120     125
Glu Ser Leu Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu
130     135     140
Lys Thr Leu Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn
145     150     155     160
Lys Cys Ile Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu
165     170     175
Val Leu Asn Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr
180     185     190
Ser Ile Leu Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile
195     200     205
Lys Lys Ser Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp
210     215     220
Tyr Arg Leu Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys
225     230     235     240
Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro
245     250

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

```

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1      5      10      15
Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
20      25      30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
35      40      45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
50      55      60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu

```

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```

65          70          75          80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
      85          90          95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
      100         105         110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
      115         120         125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
      130         135         140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
      145         150         155
His Val Lys Phe Ile Tyr Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
      165         170         175
Ile Leu Gly Gln Leu Gln Ile Phe Ser
      180         185

```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

```

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
1          5          10          15
Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
      20          25          30
Phe Glu Lys Gly Met
      35

```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

452

```

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1          5          10          15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
20          25          30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
35          40          45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
50          55          60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65          70          75          80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
85          90

```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

```

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1          5          10          15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
20          25          30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
35          40          45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
50          55          60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65          70          75          80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
85          90

```

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

```

Val Gly Lys Ser Leu Arg Tyr Ser Leu Asn Leu Asp Leu Asn Gln Lys
1          5          10          15
Ala Asp Leu Phe Thr Glu Leu Glu Pro Thr Gly Leu Thr Leu Ser
20          25          30
Pro Ile Met Lys Arg Phe Thr Ile Lys Gly Asp Phe Asp Ser Gly Leu
35          40          45
Lys Ser Tyr Asp Met Ser Tyr Met Tyr Ala Ser Leu Gln Ala Ile Ser
50          55          60
Ala Ile Arg Arg Leu Pro Leu Gly Leu Tyr Asp Gly Val His Val Tyr
65          70          75          80
Ser Lys Thr Pro Met Lys Asp Ile Glu Lys Leu Arg Asn Ala Leu Lys
85          90          95
Thr Ile Asn His Gly Ile Gly Ile Glu Gly Trp Trp Gln Gln Asn
100          105          110
Gly Asn Phe Phe Ser Ala Met Glu Leu Glu Lys Arg Ala Leu Phe Ile
115          120          125
Val Leu Met Leu Ile Ile Leu Met Ala Ser Leu Asn Ile Ile Ser Ser
130          135          140
Leu Leu Met Val Val Met Asn Arg Arg Lys Glu Ile Ala Leu Leu Phe
145          150          155          160
Ser Met Gly Ser Ser Gln Lys Glu Ile Gln Lys Thr Phe Phe Tyr Leu
165          170          175
Gly Asn Ile Ile Ser Leu
180

```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

```

Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Ile
1          5          10          15
Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro
20          25          30
His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly
35          40          45
Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp
50          55          60
Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val
65          70          75          80
Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu Pro Thr Asn His
85          90          95
Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His
100          105          110
Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala
115          120          125

```

454

```

His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu Val Leu Ala Ile
 130          135          140
Gly Phe Glu Glu Gly Lys Glu Asn Pro Asn Leu Asp Pro Ile Leu Glu
145          150          155          160
Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala Phe
          165          170          175
Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr Ala
          180          185          190
Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro Leu
          195          200          205
Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys Asn
210          215          220
Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile Ile
225          230          235          240
Lys Ser Ser Ala Glu Thr Arg
          245

```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

```

Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr Leu Ala Leu Gly
 1          5          10          15
Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe Phe Asp Asp Lys
          20          25          30
Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu Cys Tyr Pro Ser
          35          40          45
Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile Val Ser Pro Gly
50          55          60
Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys His Leu Met Ser
65          70          75          80
Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser Phe Thr Pro Thr
          85          90          95
Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr Thr Thr Glu Met
100          105          110
Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser Gly Gly Asn Ile
115          120          125
Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser Pro Leu Trp Val
130          135          140
Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn Lys Ala Tyr Pro
145          150          155          160
Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His Leu Thr Trp His
          165          170          175
Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys Val Leu Thr Leu
180          185          190
Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys Phe Lys Glu His
195          200          205
Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe Phe Asp Lys Ser

```

455

210	215	220
Glu Glu Val Leu Glu Cys Leu Lys Ile Pro Ser Asn Ala Leu Phe Phe		
225	230	235
Lys Gly Ala Phe Leu Leu Asp Ala Ala Leu Ala Leu Leu Val Tyr Glu		240
	245	250
Gln Phe Leu Lys Ile Lys Asn Leu Lys Trp Gln Asp Tyr Arg Glu Asn		255
	260	265
Ala Leu Lys Arg Leu Asn Ala Phe Lys Ile Gly Ser His Lys Met Glu		270
	275	280
Glu Phe Arg Asp Lys Gln Gly Arg Leu Trp Val Asp Asp Ser Lys Ala		285
	290	295
Thr Asn Ile Asp Ala Thr Leu Gln Ala Leu Lys Thr Phe Lys Asn Gln		300
305	310	315
Lys Ile His Leu Ile Leu Gly Gly Asp Ile Lys Gly Val Asn Leu Thr		320
	325	330
Pro Leu Phe Glu Glu Phe Lys Asn Tyr Lys Ile Ser Leu Tyr Ala Ile		335
	340	345
Gly Ser Ser Ala Ser Ile Ile Gln Ala Leu Ala Leu Glu Phe Asn Val		350
	355	360
Ser Cys Gln Val Cys Leu Lys Leu Glu Lys Ala Val Gln Glu Ile Lys		365
	370	375
Ser Val Leu Leu Gln Asn Glu Val Ala Leu Leu Ser Pro Ser Ala Ala		380
385	390	395
Ser Leu Asp Gln Phe Ser Ser Tyr Lys Glu Arg Gly Glu Lys Phe Lys		400
	405	410
Ala Phe Val Leu Lys Asp		415
	420	

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

Met	Ala	His	His	Unk	Glu	Gln	His	Gly	Gly	His	His	His	His	His	His
1				5				10					15		
His	Thr	His	His	His	His	Tyr	His	Gly	Gly	Glu	His	His	His	His	His
				20				25					30		
His	Ser	Ser	His	His	Glu	Glu	Gly	Cys	Cys	Ser	Thr	Ser	Asp	Ser	His
				35				40					45		
His	Gln	Glu	Glu	Gly	Cys	Cys	His	Gly	Unk	His	Glu				
				50				55			60				

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

456

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

Met	Ala	His	His	Unk	Glu	Gln	His	Gly	Gly	His	His	His	His	His	His
1				5				10					15		
His	Thr	His	His	His	His	Tyr	His	Gly	Gly	Glu	His	His	His	His	His
			20					25					30		
His	Ser	Ser	His	His	Glu	Glu	Gly	Cys	Cys	Ser	Thr	Ser	Asp	Ser	His
			35				40					45			
His	Gln	Glu	Glu	Gly	Cys	Cys	His	Gly	Unk	His	Glu				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550

Met	Lys	Glu	Ile	Ile	Val	Ala	Leu	Val	Gly	Gln	Pro	Asn	Val	Gly	Lys
1				5				10					15		
Ser	Ser	Leu	Ile	Asn	Ala	Leu	Ser	Asn	Thr	His	Leu	Lys	Val	Gly	Asn
			20					25				30			
Phe	Thr	Glu	Val	Thr	Val	Asp	Lys	Met	Glu	Val	Ser	Leu	Ile	Gln	Lys
			35				40					45			
Asp	His	Gln	Ile	Asn	Ser										
	50														

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

457

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1      5      10      15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
      20      25      30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
      35      40      45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
      50      55      60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
      65      70      75      80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
      85      90      95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
      100     105     110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
      115     120     125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
      130     135     140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
      145     150     155     160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
      165     170     175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
      180     185     190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
      195     200     205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
      210     215     220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
      225     230     235     240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
      245     250     255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
      260     265     270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
      275     280     285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
      290     295

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1      5      10      15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
20      25      30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
35      40      45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
50      55      60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65      70      75      80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
85      90      95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
100     105     110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
115     120     125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
130     135     140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145     150     155     160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
165     170     175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
180     185     190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
195     200     205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
210     215     220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225     230     235     240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
245     250     255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
260     265     270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
275     280     285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
290     295

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser

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```

1           5           10           15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
      20           25           30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
      35           40           45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
      50           55           60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
      65           70           75           80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
      85           90

```

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

```

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1           5           10           15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
      20           25           30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
      35           40           45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
      50           55           60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
      65           70           75           80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
      85           90

```

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...111

460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553

```

Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn Arg Ala Arg
1          5          10          15
Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val Thr Trp Trp
          20          25          30
Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser Leu Val Ser
          35          40          45
Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe Ser Leu Ser
          50          55          60
Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg Ser Leu Ala
65          70          75          80
Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe Ser Val Phe
          85          90          95
Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Leu Phe Cys His Asn
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

```

Met Gln Lys Met Gly Val Val Ser Tyr Ser Val Phe Gln Ala Phe Glu
1          5          10          15
Lys Ala Leu Ser Arg Phe Lys Glu Gly Val Val Leu Ile Val Asp Ser
          20          25          30
Leu Arg Arg Leu Ile Met Gly Ser Ala Ser Val Lys Glu Leu Ser Gly
          35          40          45
Val Ile Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser Val Ser Met
          50          55          60
Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly Ile Leu Asn
65          70          75          80
Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu Gly Val Val
          85          90          95
Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro Ile Gln Asn Ala
          100          105          110
Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val Met Phe Leu Gly
          115          120          125
Leu Phe Asn Asp Ile Thr Arg Leu Leu
          130          135

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

461

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555

```

Val Met Ala Leu Leu Lys Ile Ser Val Val Val Pro Glu Gly Glu Val
1      5      10      15
Tyr Thr Gly Glu Val Lys Ser Val Val Leu Pro Gly Val Glu Gly Glu
20     25     30
Phe Gly Val Leu Tyr Gly His Ser Asn Met Ile Thr Leu Leu Gln Ala
35     40     45
Gly Val Val Glu Ile Glu Thr Glu Asn Gln Lys Glu His Ile Ala Ile
50     55     60
Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu Arg Val Asp Ile Leu Ala
65     70     75     80
Asp Gly Ala Val Phe Ile Lys Lys Gly Ser Asp Asp Arg Asp Asp Ala
85     90     95
Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp Ala Ser Ser Asp Arg Leu
100    105    110
Ala Val Ser Ser Val Leu Ala Lys Ile Glu Ser Leu
115    120

```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556

```

Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1      5      10      15
Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
20     25     30
Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
35     40     45
Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
50     55     60
Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65     70     75     80
Ile Ser Gln Ala Ile Ile
85

```

462

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1      5      10      15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
      20      25      30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
      35      40      45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
      50      55      60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
      65      70      75      80
Pro Met Lys Ile Gln Lys
      85

```

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1      5      10      15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
      20      25      30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
      35      40      45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
      50      55      60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
      65      70      75      80
Pro Met Lys Ile Gln Lys

```

463

85

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558

```

Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1      5      10      15
Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
20      25      30
Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
35      40      45
Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
50      55      60
Gln Lys Val Thr Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65      70      75      80
Lys Phe Asp Asp Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
85      90      95
Gly Ile Asn Ala Met Trp Gly Ile Gln Asn Leu Leu
100      105

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

```

Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
1      5      10      15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
20      25      30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
35      40      45

```

464

```

Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
 50          55          60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
 65          70          75          80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
          85          90          95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
          100          105          110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
          115          120          125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
 130          135          140

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

```

Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
 1          5          10          15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
          20          25          30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
          35          40          45
Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
 50          55          60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
 65          70          75          80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
          85          90          95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
          100          105          110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
          115          120          125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
 130          135          140

```

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

465

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

```

Met Ile Asp Asn Leu Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys
1           5           10           15
Ala Tyr Ala Phe Leu Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala
20          25          30
Leu Arg Met Thr His Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile
35          40          45
Gly Asn Leu Gly Phe Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp
50          55          60
Phe Leu Gln Asp Leu Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu
65          70          75          80
Ala Leu Glu Gly Arg Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu
85          90          95
Ile Val Ile Ala Lys Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala
100         105         110
Cys Ala Gly His Thr Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile
115         120         125
Ile Ala Thr Pro Leu Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly
130         135         140
Pro Ile Val His Ala Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys
145         150         155         160
Asp Phe Ser Leu Thr Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys
165         170         175
Leu Ser Phe Cys Ala His Glu Asp Ala Leu Val Val Ile Asp Gly Gln
180         185         190
Ala Thr Tyr Asp Leu Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser
195         200         205
Pro Thr Thr Thr Lys Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys
210         215         220
Val Leu Lys Glu Lys Leu Leu
225         230

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1           5           10           15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
20          25          30

```

466

```

Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
  35          40          45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
  50          55          60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
  65          70          75          80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
          85          90          95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
          100          105          110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
          115          120          125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
          130          135          140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
          145          150          155          160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
          165          170          175
Cys Lys Lys Lys Asn Thr Ser Ser Arg
          180          185

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
  1          5          10          15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
          20          25          30
Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
          35          40          45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
          50          55          60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
          65          70          75          80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
          85          90          95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
          100          105          110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
          115          120          125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
          130          135          140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
          145          150          155          160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
          165          170          175
Cys Lys Lys Lys Asn Thr Ser Ser Arg

```

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180

185

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562

```

Met Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu
1           5           10           15
Ala His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met
          20           25           30
Arg Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile
          35           40           45
Leu Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu
          50           55           60
Glu Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val
          65           70           75           80
Gly Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu
          85           90           95
Phe Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val
          100          105          110
Pro Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile
          115          120          125
Gly Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe
          130          135          140
Leu Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val
          145          150          155          160
Leu Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu
          165          170          175
Ala Leu Gln Gln Leu Arg Ser
          180

```

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563

```

Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn Asn Leu
1      5      10      15
Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala Ile Ala
20      25      30
Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro Leu Lys
35      40      45
Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu Asp Ala
50      55      60
Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala Ser Phe
65      70      75      80
Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys Lys Gln
85      90      95
Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly Val Ser
100      105      110
Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile Pro Leu
115      120      125
Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe Val Ala
130      135      140
Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
145      150

```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564

```

Val Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser
1      5      10      15
Phe Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser
20      25      30
Lys Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr
35      40      45
Ile Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala
50      55      60
Phe Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn
65      70      75      80
Ser Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu
85      90      95
Leu Ser Tyr Pro Asn Asp Pro Asn Asn Glu Asp Asn Ala Asn Asn
100      105      110
Ser Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn
115      120      125
Pro Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn
130      135      140
Gly Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile

```

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145		150		155		160
Gln Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp						
	165		170		175	
Arg Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala						
	180		185		190	
Gln Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly						
	195		200		205	
Ser Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys						
	210		215		220	
Ser Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu						
	225		230		235	
Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu						
	245		250		255	
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu						
	260		265		270	
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser						
	275		280		285	

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565

Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser Asn Pro Leu Val																			
1			5				10				15								
Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr Leu Tyr Pro Asn																			
			20				25				30								
Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu Tyr Ser Glu Ile																			
			35				40				45								
Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu Lys Gly Ile Gly																			
			50				55				60								
Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met Val Leu Gly Met																			
			65				70				75								
Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln Asn Asn Asp Leu																			
			85				90				95								
Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe Val Gly Tyr Leu																			
			100				105				110								
Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser Ser Ser Gly Asn																			
			115				120				125								
Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr Glu Ile Phe Asp																			
			130				135				140								
Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn Val Val Lys Glu																			
			145				150				155								
Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile Asp Thr His His																			
			165				170				175								
Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg Gln Ile Leu Thr																			
			180				185				190								
Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn Asn Gly Leu Ser																			
			195				200				205								

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```

Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val Ile Leu Gly Leu
 210                215                220
Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val Phe Met Thr Tyr
225                230                235                240
Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe Met Leu Leu Leu
                245                250                255
Gly Phe Phe Gln Thr Arg Gly Phe Leu Val Ser Tyr Val Lys Lys
                260                265                270
Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu Leu Leu Val Leu
                275                280                285
Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val Gly Gly Ser Asn
290                295                300
Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile Gly Ile Ser Leu
305                310                315                320
Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala Ile Phe Gly Thr
                325                330                335
Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr Gln Gly Val Gln
                340                345                350
Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser Leu Lys Ser Val
                355                360                365
Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr Lys Asp Ala Lys
370                375                380
Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp Met Pro Gly His
385                390                395                400
Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu Pro Lys Ser His
                405                410                415
Arg Ala Ser Lys
                420

```

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566

```

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
 1                5                10                15
Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
                20                25                30
Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
                35                40                45
Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
                50                55                60
Gln Val Asn Tyr Lys Ser Ala Pro
65                70

```

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

```

Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly
1          5          10          15
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly
20          25          30
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu
35          40          45
Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser
50          55          60
Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro
65          70          75          80
Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro Leu
85          90          95
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu
100         105         110
Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu Gln
115         120         125
Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu
130         135         140
Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys
145         150         155         160
Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala
165         170         175
Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser
180         185         190
Lys Ala Phe His Phe Met Leu Ile Ser Ser Gln Lys Ile
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568

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```

Met Glu Lys Val Cys Val Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu
1      5      10      15
Glu Arg Leu Lys Glu Lys Tyr Gly Asp Asp Trp Glu Lys His Val Lys
20      25      30
Ala Lys Ala Ile Asn Glu Glu Leu Glu Glu Gln Val Lys Ala Lys
35      40      45
Ala Lys Glu Gln Gln Lys Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe
50      55      60
Leu Lys Lys Val Gly Leu Lys Lys Arg Asp Met Leu Gln Ser Thr Met
65      70      75      80
Leu Phe Asp Glu Val Lys Glu Ala Asp Val Leu Phe Gln Ala Glu Arg
85      90      95
Lys Ile Gly Asp Trp Ile Phe Ser Ser Ala Val Phe Phe Phe Ala Leu
100     105     110
Ala Leu Ile Glu Ala Ile Ile Ile Val Cys Leu Leu Pro Leu Lys Glu
115     120     125
Lys Val Pro Tyr Leu Val Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala
130     135     140
Ile Val Gln Arg Ala Asp Lys Ser Ile Arg Ala Asn Gln Ala Leu Val
145     150     155     160
Arg Gln Leu Val Ala Ser Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser
165     170     175
Ile Lys Glu Gln Asn Glu Ile Ala His Glu Thr Ile Arg Leu Gln Ser
180     185     190
Ala Phe Glu Val Trp Asp Phe Phe Glu Lys Leu Val Ser Tyr Glu His
195     200     205
Ser Ile Tyr Thr Asn Ile Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn
210     215     220
Ile Ala Leu Ile Ser Lys Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln
225     230     235     240
Leu Phe His Lys Glu Lys Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile
245     250     255
Met Thr Phe Glu Phe Glu Pro Ile Glu Ile Asp Thr Lys Ser Val Pro
260     265     270
Leu Asn Pro Thr Gly Phe Ile Val Thr Gly Tyr Asp Val Thr Glu Ile
275     280     285
Ala Ile Leu Lys Asp Leu Asp Glu Lys Asn Lys Val Lys Asp Asp Gly
290     295     300
Val Lys Ser Arg Ile Ile His Val Glu Lys Lys Asp Pro His Met Ser
305     310     315     320
Gln Tyr Lys Asp Val Lys Glu Gln
325

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn

473

```

1           5           10           15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
20           25           30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Asp Glu
35           40           45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
50           55           60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65           70           75           80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
85           90           95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
100          105          110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
115          120          125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
130          135

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

```

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
1           5           10           15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
20           25           30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Asp Glu
35           40           45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
50           55           60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65           70           75           80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
85           90           95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
100          105          110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
115          120          125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
130          135

```

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570

```

Met Leu His Lys Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly
 1             5             10             15
Ile Phe Cys Val Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met
      20             25             30
Val Ala Phe Lys Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly
      35             40             45
Ser Val Val Phe Leu Trp Ser Asp Leu Leu Val Phe Val Gly Phe Lys
 50             55             60
Asn Ile Ser Phe Val Leu Asp Ile Gly Tyr Glu Ile
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
 1             5             10             15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
      20             25             30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
      35             40             45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
 50             55             60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65             70             75             80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
      85             90             95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
      100            105            110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
      115            120            125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
      130            135            140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu

```

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```

145          150          155          160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
          165          170          175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
          180          185          190
Phe

```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1          5          10          15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
          20          25          30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
          35          40          45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
          50          55          60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
          65          70          75          80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
          85          90          95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
          100          105          110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
          115          120          125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
          130          135          140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
          145          150          155          160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
          165          170          175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
          180          185          190
Phe

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

```

Met Pro Phe Leu Lys Asn Trp Ile Trp Ser Leu Lys Met Ala Leu Ser
1          5          10          15
Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
20          25          30
Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
35          40          45
Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
50          55          60
Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
65          70          75          80
Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
85          90          95
Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
100         105         110
Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
115         120         125
Tyr Ile Gln Asn Lys Asn Lys Arg Leu Ala Pro Phe
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

```

Met Pro Gln Asn Gln Leu Val Ile Thr Ile Ile Asp Glu Ser Gly Ser
1          5          10          15
Lys Gln Leu Lys Phe Ser Lys Asn Leu Lys Arg Asn Leu Ile Ile Ser
20          25          30
Val Val Ile Leu Leu Leu Ile Val Gly Leu Gly Val Gly Phe Leu Lys
35          40          45
Phe Leu Ile Ala Lys Met Asp Thr Met Thr Ser Glu Arg Asn Ala Val
50          55          60
Leu Arg Asp Phe Arg Gly Leu Tyr Gln Lys Asn Tyr Ala Leu Ala Lys
65          70          75          80
Glu Ile Lys Asn Lys Arg Glu Glu Leu Phe Ile Val Gly Gln Lys Ile
85          90          95
Arg Gly Leu Glu Ser Leu Ile Glu Ile Lys Lys Gly Ala Asn Gly Gly

```

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```

      100      105      110
Gly His Leu Tyr Asp Glu Val Asp Leu Glu Asn Leu Ser Leu Asn Gln
      115      120      125
Lys His Leu Ala Leu Met Leu Ile Pro Asn Gly Met Pro Leu Lys Thr
      130      135      140
Tyr Ser Ala Ile Lys Pro Thr Lys Glu Arg Asn His Pro Ile Lys Lys
      145      150      155      160
Ile Lys Gly Val Glu Ser Gly Ile Asp Phe Ile Ala Pro Leu Asn Thr
      165      170      175
Pro Val Tyr Ala Ser Ala Asp Gly Ile Val Asp Phe Val Lys Thr Arg
      180      185      190
Ser Asn Ala Gly Tyr Gly Asn Leu Val Arg Ile Glu His Ala Phe Gly
      195      200      205
Phe Ser Ser Ile Tyr Thr His Leu Asp His Val Asn Val Gln Pro Lys
      210      215      220
Ser Phe Ile Gln Lys Gly Gln Leu Ile Gly Tyr Ser Gly Lys Ser Gly
      225      230      235      240
Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe Leu Gly Lys
      245      250      255
Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp His Phe Gln
      260      265      270
Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn Leu Phe Trp
      275      280      285
Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp Lys Asp Thr
      290      295      300
Leu Lys Gly Gln
      305

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574

```

Met Ile Thr Gly Ser His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile
1      5      10      15
Thr Leu Asn Gln Asn Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys
      20      25      30
Asn Thr Leu Leu Asn Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr
      35      40      45
Pro Glu Lys Val Asn Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys
      50      55      60
Asp Phe Lys His Leu Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe
      65      70      75      80
Gly Asn Gly Val Gly Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu
      85      90      95
Asn Ile Asp Phe Ser Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro
      100      105      110
Asn His His Pro Asp Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu
      115      120      125

```

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```

Lys His Met Arg Glu Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly
 130          135          140
Asp Ala Asp Arg Ile Ala Met Leu Ser Ser His His Ile Tyr Ala Gly
145          150          155          160
Asp Glu Leu Ala Ile Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile
          165          170          175
Thr Pro Phe Val Ile Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn
          180          185          190
Ala Ile Asn Thr Phe Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser
          195          200          205
Asn Leu Lys Ile Lys Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu
210          215          220
Met Ser Gly His Ile Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp
225          230          235          240
Ala Leu Tyr Ala Cys Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser
          245          250          255
Pro Ser Asp Leu Glu Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr
          260          265          270
Thr Pro Glu Glu Lys Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile
275          280          285
Ile Arg Asn Leu Gln Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro
290          295          300
Thr Ile Lys Glu Ile Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu
305          310          315          320
His Gly Phe Gly Leu Ile Arg Ala Ser Asn Thr His Pro Leu Phe Ser
          325          330          335
Gln Pro Leu

```

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575

```

Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Unk Pro Gln
 1          5          10          15
Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala Phe
          20          25          30
Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile Thr
          35          40          45
Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met Val
          50          55          60
Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly Val
65          70          75          80
Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala Phe
          85          90          95
Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys Gln
          100          105          110
Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu Leu

```

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Thr	Leu	Ile	Leu	Ser	Ala	Pro	Ser	Ile	Unk	Glu	Asn	Leu	Ser	Lys	Gln
130						135					140				
Val	Asn	Ser	Asn	Ala	Ile	Asp	Ala	Gln	Unk	Pro	Asn	Ile	Lys	Ala	Ile
145					150					155					160
Gly	Tyr	Val	Leu	Phe	Thr	Asn	Tyr	Leu	Ile	Pro	Phe	Glu	Ala	Ala	Ala
				165				170						175	
Leu	Met	Leu	Leu	Val	Ala	Met	Val	Gly	Gly	Ile	Ala	Thr	Gly	Ile	Gln
				180				185				190			
Lys	Ile	His	Gly	Lys	Asn	His	Thr	Gln	Phe	Ile	Lys	Glu	Ser	Leu	
	195					200						205			

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576

Met	Gly	Ala	Ile	Leu	Ser	Ile	Leu	Lys	Leu	Glu	Ile	Lys	Ser	Tyr	Leu
1			5						10					15	
Thr	Asn	Thr	Ser	Ala	Leu	Phe	Trp	Thr	Phe	Ile	Tyr	Pro	Ile	Leu	Met
			20				25						30		
Leu	Leu	Leu	Leu	Ile	Phe	Val	Phe	Ser	Lys	Asn	Thr	Thr	Glu	Ile	Phe
			35			40					45				
Tyr	Phe	Asn	Asn	Ile	Ile	Gly	Leu	Met	Gly	Leu	Leu	Ile	Ile	Ser	Ser
		50			55				60						
Ala	Ile	Phe	Gly	Leu	Thr	Gln	Ala	Ile	Thr	Ser	Ser	Arg	Ser	His	Asn
65				70					75					80	
Ile	Phe	Leu	Phe	Tyr	Met	Leu	Ser	Pro	Ala	Thr	Phe	Lys	Gln	Ile	Thr
			85					90					95		
Leu	Ala	Leu	Ile	Ala	Ser	Arg	Leu	Ile	Val	Val	Ile	Leu	Tyr	Ala	Phe
			100				105					110			
Ile	Phe	Ile	Val	Leu	Ser	Phe	Tyr	Ala	Leu	Asn	Ile	Ile	Thr	Ile	Leu
			115			120					125				
Asn	Phe	Lys	Ala	Leu	Ile	Leu	Gly	Phe	Ile	Ser	Ile	Phe	Ser	Ser	Ala
		130			135					140					
Leu	Phe	Cys	Phe	Cys	Leu	Ala	Ile	Phe	Val	Ala	Arg	Ile	Phe	Gln	Asn
145				150					155					160	
Glu	Gln	Ser	Ile	Leu	Gly	Phe	Cys	Asn	Ile	Ile	Asn	Leu	Tyr	Ala	Leu
			165					170					175		
Met	Ser	Cys	Asn	Val	Phe	Val	Pro	Leu	Glu	Tyr	Leu	Pro	Asn	Ile	Gly
			180				185					190			
Gln	Leu	Phe	Ile	Lys	Thr	Ser	Ile	Phe	Tyr	Tyr	Leu	Asn	Gln	Leu	Leu
			195			200					205				
Ile	Lys	Ala	Phe	Gln	Gly	Ile	Asp	Thr	Ile	Leu	Val	Leu	Ala	Thr	Ser
		210			215					220					
Thr	Phe	Phe	Ile	Ile	Gly	Gly	Ile	Ile	Leu	Phe	Leu	Leu	Ser	Ala	Asn
225				230					235					240	
Arg	Met	Leu	Leu	Thr	Pro	Lys	Glu	Arg	Met	Arg					
			245					250							

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(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577

```

Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu
 1             5             10             15
Ser Gln Val Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro
      20             25             30
Phe Ala Gly Ile Val Ala Gly Ala Met Thr Ala Ala Ile Ile Pro Ile
      35             40             45
Val Val Gly Phe Thr Asn Pro Gln Met Thr Asp Ile Ile Asn Pro Ile
      50             55             60
Lys Ser Lys His Arg
65

```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

```

Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys
 1             5             10             15
Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val
      20             25             30
Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu
      35             40             45
Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu
      50             55             60
Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys
      65             70             75             80
Lys Leu Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser

```


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				85				90					95				
Val	Gly	Val	Asn	Ala	Met	Ile	Leu	Ser	Leu	Leu	Tyr	Lys	Lys	Pro	Pro		
			100					105					110				

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579

[illegible]

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...129

482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

```

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1           5           10           15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
           20           25           30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
           35           40           45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
           50           55           60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65           70           75           80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
           85           90           95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
           100          105          110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
           115          120          125
Pro

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

```

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1           5           10           15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
           20           25           30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
           35           40           45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
           50           55           60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65           70           75           80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
           85           90           95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
           100          105          110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
           115          120          125
Pro

```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

483

(A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

```

Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg Leu Gly Tyr Glu Asp
1          5          10          15
Val Leu Glu Ala Glu His Gly Val Glu Ala Trp Glu Lys Leu Asp Ala
20          25          30
Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp Asn Met Pro Glu Met
35          40          45
Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala Asp Asn Arg Phe Lys
50          55          60
Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly Gly Lys Ala Glu Val
65          70          75          80
Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr Ile Val Lys Pro Phe
85          90          95
Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val Val Leu Gly Thr Asn
100          105          110
Asp
  
```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

```

Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser
1          5          10          15
Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu
20          25          30
Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser
35          40          45
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met
50          55          60
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr
65          70          75          80
  
```

484

```

Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn
      85                      90                      95
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu
      100                      105                      110
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr
      115                      120                      125
Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu
      130                      135                      140
Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys
145                      150                      155                      160
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn
      165                      170

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

```

Met Gly Cys Phe Ser Thr Ile Cys Cys Lys Gly Leu Thr Leu Ser Val
1      5      10      15
Gly Gly Phe Leu Val Met Met Arg Phe Leu Ile Phe Lys Asp Phe Cys
      20      25      30
Lys Asp Phe
      35

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

```

Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1      5      10      15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys

```

485

```

      20      25      30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
      35      40      45
Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
      50      55      60
Asp Ala Pro Leu Pro Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
      65      70      75      80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
      85      90      95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
      100      105      110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
      115      120      125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
      130      135      140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
      145      150      155      160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
      165      170      175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
      180      185      190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
      195      200      205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
      210      215      220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
      225      230      235      240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
      245      250      255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
      260      265      270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
      275      280      285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
      290      295      300
Tyr Leu Ala
305

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

```

Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1      5      10      15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys
      20      25      30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
      35      40      45

```

486

```

Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
 50      55      60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
 65      70      75      80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
      85      90      95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
 100     105     110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
 115     120     125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
 130     135     140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
 145     150     155     160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
      165     170     175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
 180     185     190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
 195     200     205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
 210     215     220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
 225     230     235     240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
      245     250     255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
 260     265     270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
 275     280     285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
 290     295     300
Tyr Leu Ala
305

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

```

Val Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser
 1      5      10      15
Ile Gln Ser Asp Ser Gln Tyr Leu Gln Ala Unk Leu Asn Gln Phe Glu
      20      25      30
Asn Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr
 35      40      45
His Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His
 50      55      60
Ala Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe

```

487

65					70					75					80
Leu	Gln	Glu	Thr	Leu	Lys	Ser	Leu	Glu	Ile	Gln	Leu	Lys	Asn	Tyr	Ala
				85					90					95	
Pro	Lys	Leu	Leu	Asn	Ser	Lys	Glu	Val	Leu	Asn	Phe	Tyr	Ala	Glu	Tyr
				100				105					110		
Ile	Asn	Gly	Phe	Glu	Leu	Pro	Leu	Lys	Pro	Leu	Val	Gly	Gly	Tyr	Leu
		115					120					125			
Ser	Asp	Ser	Tyr	Ile	Ala	Ser	Ser	Ile	Thr	Phe	Glu	Lys	Asp	Tyr	Phe
	130					135					140				
Ile	Gln	Glu	Ser	Phe	Asn	Gln	Lys	Thr	Tyr	Asn	Arg	Leu	Ile	Gly	Ile
145					150					155					160
Lys	Ala	Tyr	Glu	Ser	Glu	Arg	Ile	Thr	Ser	Ile	Ala	Val	Gly	Ala	Leu
				165						170				175	
Leu	Tyr	Gln	Glu	Thr	Pro	Leu	Asp	Ile	Ile	Phe	Ser	Ile	Glu	Pro	Met
				180				185					190		
Ser	Val	Asn	Lys	Thr	Leu	Ser	Phe	Leu	Lys	Glu	Arg	Ala	Lys	Phe	Ser
	195						200					205			
Met	Ser	Asn	Leu	Val	Lys	Asn	Glu	Leu	Leu	Glu	Tyr	Gln	Glu	Leu	Val
	210					215					220				
Lys	Thr	Lys	Arg	Leu	Ser	Met	Gln	Lys	Phe	Ala	Leu	Asn	Val	Leu	Ile
225						230				235					240
Lys	Ala	Pro	Ser	Leu	Glu	Asp	Leu	Asp	Ala	Gln	Thr	Ser	Leu	Ile	Leu
				245						250				255	
Gly	Leu	Leu	Phe	Lys	Glu	Asn	Leu	Val	Gly	Val	Ile	Glu	Thr	Phe	Gly
			260					265					270		
Leu	Lys	Gly	Gly	Tyr	Phe	Ser	Phe	Phe	Pro	Glu	Arg	Ile	His	Leu	Asn
	275						280					285			
His	Arg	Leu	Arg	Phe	Leu	Thr	Ser	Lys	Ala	Leu	Ala	Cys	Leu	Met	Val
	290					295					300				
Phe	Glu	Arg	Gln	Asn	Leu	Gly	Phe	Lys	Ala	Asn	Ser	Trp	Gly	Asn	Ser
305					310					315					320
Pro	Leu	Ser	Val	Phe	Lys	Asn	Leu	Asp	Tyr	Ser	Pro	Phe	Leu	Phe	Asn
				325					330					335	
Phe	His	Asn	Gln	Glu	Val	Ser	His	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Arg
			340					345					350		
Val	Asn	Gly	His	Thr	Leu	Val	Ile	Gly	Ala	Thr	Gly	Ser	Gly	Lys	Ser
	355						360					365			
Thr	Leu	Ile	Ser	Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Gln	Asn	Met
	370					375					380				
Arg	Leu	Leu	Ala	Phe	Asp	Arg	Met	Gln	Gly	Leu	Tyr	Ser	Phe	Thr	Glu
385					390					395					400
Phe	Phe	Lys	Gly	His	Tyr	His	Asp	Gly	Gln	Ser	Phe	Ser	Ile	Asn	Pro
				405					410					415	
Phe	Cys	Leu	Glu	Pro	Asn	Leu	Gln	Asn	Leu	Glu	Phe	Leu	Gln	Ser	Phe
			420					425					430		
Phe	Leu	Ser	Met	Leu	Asp	Leu	Ala	Pro	Ser	Arg	Asp	Lys	Glu	Ala	Leu
	435						440					445			
Glu	Asp	Met	Asn	Ala	Ile	Ser	Gly	Ala	Ile	Lys	Ser	Leu	Tyr	Glu	Thr
	450					455					460				
Leu	Tyr	Pro	Lys	Asp	Phe	Ser	Leu	Leu	Asp	Phe	Lys	Glu	Thr	Leu	Lys
465					470					475					480
Arg	Thr	Ser	Ser	Asn	Gln	Leu	Gly	Leu	Ser	Leu	Glu	Pro	Tyr	Leu	Asn
				485					490					495	
Asn	Pro	Leu	Phe	Asn	Ala	Leu	Asn	Asp	Ala	Phe	Asn	Ser	Asn	Ala	Phe
			500					505					510		
Leu	Asn	Val	Ile	Asn	Leu	Asp	Ala	Ile	Thr	Gln	Asn	Pro	Lys	Asp	Leu
	515						520					525			
Gly	Leu	Leu	Ala	Tyr	Tyr	Leu	Phe	Tyr	Lys	Ile	Leu	Glu	Glu	Ser	Arg
	530					535					540				
Lys	Asn	Asp	Ser	Gly	Phe	Leu	Val	Phe	Leu	Asp	Glu	Phe	Lys	Ser	Tyr
545					550					555					560
Val	Glu	Asn	Asp	Leu	Leu	Asn	Thr	Lys	Ile	Asn	Ala	Leu	Ile	Thr	Gln
				565					570					575	
Ala	Arg	Lys	Ala	Asn	Gly	Val	Val	Val	Leu	Ala	Leu	Gln	Asp	Ile	Tyr
			580					585					590		

SUBSTITUTE SHEET (RULE 26)

488

Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
 595 600 605
 Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
 610 615 620
 Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
 625 630 635 640
 Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
 645 650 655
 Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
 660 665 670
 Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
 675 680 685
 Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
 690 695 700

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586

Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser
 1 5 10 15
 Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala
 20 25 30
 Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Unk
 35 40 45
 Tyr Leu Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile
 50 55 60
 Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala
 65 70 75 80
 Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln
 85 90 95
 Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp
 100 105 110
 Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn
 115 120 125
 Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile
 130 135 140
 Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu
 145 150 155 160
 Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala
 165 170 175
 Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg
 180 185 190
 Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg
 195 200 205
 Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn
 210 215 220
 Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys

489

```

225          230          235          240
Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
          245          250          255
Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
          260          265          270
Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
          275          280          285
Asn Lys Lys Gln Phe
          290

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

```

Met Pro Lys Ser Phe Thr Leu Pro Thr Phe Val Trp Cys Leu Phe Val
1          5          10          15
Gly Val Ile Leu Arg Asn Ala Leu Ser Phe Phe Lys Ile His Ser Val
          20          25          30
Phe Asp Arg Glu Val Ser Val Ile Gly Asn Val Ser Leu Ser Leu Phe
          35          40          45
Leu Ala Tyr Ala
          50

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588

```

Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile Leu
1          5          10          15
Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu Ser
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

490

```

Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys Ala
      35      40      45
Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu Val
      50      55      60
Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser Gly
      65      70      75      80
Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys Pro
      85      90      95
Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser Ile
      100      105      110
Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln Asp
      115      120      125
Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala Phe
      130      135      140
Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr Gly
      145      150      155      160
Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys Arg
      165      170      175
Leu Leu Glu Ser Arg Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

```

Val Ser Leu Ile Lys Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser
1      5      10      15
Ile Pro Leu Thr Ser Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His
      20      25      30
Ala Phe Ser Asp Tyr Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe
      35      40      45
Ser Leu Lys His Tyr Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile
      50      55      60
Lys Asp Lys Glu Lys Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr
      65      70      75      80
His Phe Leu Gly Ala Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser
      85      90      95
Glu Met Ile Tyr Tyr Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn
      100      105      110
Leu Glu Asn Thr Leu Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu
      115      120      125
Asp Asn Phe Met Ile Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly
      130      135      140
Gly Met Asp Phe Glu Leu Ser Arg Ile Ser Tyr Pro Leu Leu Ile His
      145      150      155      160
Ser Phe Asp Asp Asn Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln
      165      170      175
Tyr Gly Ser Lys Thr Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu

```

491

```

      180              185              190
Glu Leu Lys Thr Ala Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys
      195              200              205
Glu His Ala Leu Leu Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu
      210              215              220
Glu Met Leu Lys Ile Phe Gly Leu Leu Ser Gln Val His His Asn Asp
      225              230              235              240
Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn
      245              250

```

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

```

Val Ile Thr Ala Cys Phe Asn Arg Glu Lys Thr Ile Glu Asp Thr Ile
1           5           10           15
Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile Glu Tyr Ile Ile Ile
      20           25           30
Asp Gly Ala Ser Ala Ile Ala Leu
      35           40

```

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591

```

Val Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe
1           5           10           15
Glu Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr
      20           25           30
Ile Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala
      35           40           45

```

492

```

Arg Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys
 50          55          60
Glu Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn
 65          70          75          80
Gly Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys
          85          90          95
Tyr Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Glu
          100          105          110
Lys Leu His Val Trp Leu Cys Gln Ile Tyr
          115          120

```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592

```

Met Lys Arg Leu Ala Val Ala Leu Ile Leu Val Leu Gly Val Val Trp
 1          5          10          15
Gly Lys Ser Leu Pro Lys Trp Ala Lys Asp Cys Ser Lys Glu Met Arg
          20          25          30
Ile Glu Lys Thr Gln Thr Lys Asp Glu Lys Ile Leu Val Cys Gly Met
          35          40          45
Ser Asp Ile Leu Leu Ser Asp Met Asp Tyr Ser Leu Ser Ser Ala Arg
 50          55          60
Gln Asn Ala Leu Glu Lys Val Met Glu Ala Phe Lys Gly Asp Arg Ile
 65          70          75          80
Glu Ile Lys Ala Gly Glu Leu Lys Ala Thr Phe Ile Asp Thr Asp Lys
          85          90          95
Val Tyr Val Leu Leu Arg Ile Thr Lys Lys His Val Ala Leu Met Asn
          100          105          110
Glu

```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

493

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

```

Met Asn Pro Gln Ile Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu
1      5      10      15
Leu Ala Ala Ser Ser Gly Asn Leu Val Glu Trp Tyr Asp Phe Tyr Ala
      20      25      30
Tyr Ala Phe Leu Ala Pro Tyr Phe Ala Lys Glu Phe Thr His Thr Asn
      35      40      45
Asp Pro Thr Leu Ala Leu Ile Ser Ala Phe Leu Val Phe Met Leu Gly
50      55      60
Phe Phe Met Arg Pro Leu Gly Ser Leu Phe Phe Gly Lys Leu Gly Asp
65      70      75      80
Lys Lys Gly Arg Lys Thr Ser Met Val Tyr Ser Ile Ile Leu Met Ala
      85      90      95
Leu Gly Ser Phe Met Leu Ala Leu Leu Pro Thr Lys Glu Ile Val Gly
      100      105      110
Glu Trp Ala Phe Leu Phe Leu Leu Ala Arg Leu Leu Gln Gly Phe
      115      120      125
Ser Val Gly Gly Glu Tyr Gly Val Val Ala Thr Tyr Leu Ser Glu Leu
130      135      140
Gly Lys Asn Gly Lys Lys Gly Phe Tyr Gly Ser Phe Gln Tyr Val Thr
145      150      155      160
Leu Val Gly Gly Gln Leu Leu Ala Ile Phe Ser Leu Phe Ile Val Glu
      165      170      175
Asn Val Tyr Thr His Glu Gln Ile Ser Ala Phe Ala Trp Arg Tyr Leu
180      185      190
Phe Ala Leu Glu Gly Ile Leu Ala Leu Leu Ser Leu Phe Leu Arg Asn
195      200      205
Ile Met Glu Glu Thr Met Asp Asn Glu Ala Thr Pro Gln Lys Lys Thr
210      215      220
Asn Val Asn Asn Thr Lys Glu Thr His Ile Lys Glu Thr Gln Arg Gly
225      230      235      240
Ser Leu Lys Glu Leu Asn His Lys Lys Ala Leu Met Ile Val Phe
      245      250      255
Gly Leu Thr Met Gly Gly Ser Leu Cys Phe Tyr Thr Phe Thr Val Tyr
260      265      270
Leu Lys Ile Phe Leu Thr Asn Ser Ser Phe Ser Pro Lys Glu Ser
275      280      285
Ser Phe Ile Met Leu Leu Ala Leu Ser Tyr Phe Ile Phe Leu Gln Pro
290      295      300
Leu Cys Gly Met Leu Ala Asp Lys Ile Lys Arg Thr Gln Met Leu Met
305      310      315      320
Val Phe Ala Ile Thr Gly Leu Ile Val Thr Pro Ile Val Phe Tyr Gly
      325      330      335
Ile Lys His Ala Thr Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu
340      345      350
Ala Leu Ser Ser Met Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys
355      360      365
Ala Glu Leu Phe Pro Glu His Val Arg Ala Leu Gly Val Gly Leu Ala
370      375      380
Tyr Ala Ile Ala Asn Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala
385      390      395      400
Leu Glu Phe Lys Gln His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val
      405      410      415
Met Leu Ser Ile Val Ile Phe Met Val Met Val Ile Ile Phe Pro Lys
420      425      430
Lys Thr Tyr Leu Glu
      435

```

(2) INFORMATION FOR SEQ ID NO:594:

SUBSTITUTE SHEET (RULE 26)

494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1      5      10      15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20      25      30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu
35      40      45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
50      55      60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
65      70      75      80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
85      90      95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
100     105     110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu
115     120     125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
130     135     140
Lys Ala
145

```

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1      5      10      15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20      25      30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu

```

495

```

      35              40              45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
  50              55              60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
  65              70              75
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
      85              90              95
Glu Ala Gln His Lys Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
      100              105              110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu
      115              120              125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
      130              135              140
Lys Ala
145

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
  1              5              10              15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
      20              25              30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
      35              40              45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
      50              55              60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
      65              70              75
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
      85              90              95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
      100              105              110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
      115              120              125

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

496

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
 1           5           10           15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
          20           25           30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
          35           40           45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
 50           55           60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
 65           70           75           80
Lys Ala Leu Glu Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
          85           90           95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
          100          105          110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

```

Met Asp Ile Ser Ile Phe Arg Glu Tyr Asp Ile Arg Gly Ile Tyr Pro
 1           5           10           15
Thr Thr Leu Asp Glu Asn Thr Ala Phe Ser Ile Gly Val Glu Leu Gly
          20           25           30
Lys Ile Met Arg Glu Tyr Asp Lys Ser Val Phe Val Gly His Asp Ala
          35           40           45
Arg Val His Gly Arg Phe Leu Phe Glu Val Leu Ser Ala Gly Leu Gln
 50           55           60
Ser Ser Gly Leu Lys Val Tyr Asp Leu Gly Leu Ile Pro Thr Pro Val
 65           70           75           80
Ala Tyr Phe Ala Ala Phe Asn Glu Ile Asp Asn Ile Gln Trp Pro
          85           90           95

```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

497

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

```

Val Cys Asp Ile Phe Ser Asp Gly Val Leu Leu Asp Lys Ala Leu Val
1           5           10           15
Ile Tyr Phe Lys Ala Pro Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu
20           25           30
Ile Gln Cys His Gly Ser Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala
35           40           45
Cys Leu Asn Leu Gly Ala Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys
50           55           60
Lys Ala Phe Leu Asn His Lys Met Asp Leu Ser Glu Ile Glu Ala Ser
65           70           75           80
Val Gln Leu Ile Leu Cys Glu Asp Glu Ser Val Leu Asn Ala Leu Ala
85           90           95
Arg Gln Leu Gln Gly Gly
100
  
```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

```

Met Phe Lys Lys Met Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys
1           5           10           15
Val Gly Ala Lys Asp Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly
20           25           30
Gly Lys Phe Met Gly Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr
35           40           45
Ser Met Asn Asp Glu Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg
50           55           60
Gly Asn Ser Val Glu Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp
65           70           75           80
Lys Phe Lys Lys Glu Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln
85           90           95
  
```

498

Gln Ile Phe Tyr Arg Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val
 100 105 110
 Lys Ile Ile Thr Asp Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

Met Thr Leu Lys Pro Tyr Pro Thr Lys Glu Thr Gly Leu Ala Ser Gln
 1 5 10 15
 Leu Ser Gly His Trp Phe Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn
 20 25 30
 Phe Asn Pro Asn Lys Ile Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser
 35 40 45
 Lys Ile Lys Phe Asp Lys Asp Leu Glu Ile Tyr Phe Asp Ser His Glu
 50 55 60
 Ser Phe Asn Ile Ser Lys Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser
 65 70 75 80
 Leu Lys Lys Ile Lys Gln Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile
 85 90 95
 Glu Ser Lys His Asp Asn Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu
 100 105 110
 Asn Asp Thr Ser Phe Leu Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu
 115 120 125
 Glu Tyr Asn Met Gln Leu Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe
 130 135 140
 Asn Lys Leu Leu Ala Ile Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln
 145 150 155 160
 Leu Lys Ile Arg Val Arg His Asn Asn Lys Leu Pro Arg Glu Lys Tyr
 165 170 175
 Thr Glu His Glu Ile Lys Leu Glu Val Tyr Asp Cys Arg Lys Ser His
 180 185 190
 Asp His Asn Glu Pro Ile Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln
 195 200 205
 Trp Ala Phe Asn Phe Met Phe Gly Phe Leu Tyr Asn Val Gly Ser His
 210 215 220
 Phe Ser Phe Asn His Asn Ile Ile Tyr Val Met Asp Glu Pro Ala Thr
 225 230 235 240
 His Leu Ser Val Pro Ala Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu
 245 250 255
 Tyr Ala His Lys Asn His Val Thr Phe Val Leu Ala Thr His Asp Pro
 260 265 270
 Phe Leu Val Asp Thr Asp His Leu Asp Glu Ile Arg Ile Val Glu Lys
 275 280 285
 Glu Thr Glu Gly Ser Val Ile Lys Asn His Phe Asn Tyr Pro Leu Asn
 290 295 300
 Asn Ala Ser Lys Asp Ser Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu

499

```

305          310          315          320
Gly Val Gly Gln His Val Phe His Asn Pro Gln Lys His Arg Ile Ile
          325          330          335
Phe Val Glu Gly Ile Thr Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu
          340          345          350
Tyr Leu Arg Tyr Lys Glu Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe
          355          360          365
Leu Pro Ile Ser Gly Leu Lys Asn Asp Ser Asn Asp Met Lys Glu Thr
          370          375          380
Ile Glu Lys Leu Cys Glu Leu Asp Asn His Pro Ile Val Leu Thr Asp
385          390          395          400
Asp Asp Arg Lys Cys Val Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe
          405          410          415
Lys Arg Ala Asn Glu Glu Met His Asp Pro Ile Thr Ile Leu Gln Leu
          420          425          430
Ser Asp Cys Asp Arg His Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala
          435          440          445
Asn Asp Arg Asn Lys Tyr Ala Lys Asn Lys Gln Met Glu Leu Ser Met
          450          455          460
Ala Phe Lys Thr Arg Leu Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys
465          470          475          480
Gln Thr Lys Arg Asn Phe Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala
          485          490          495
Thr Asn Leu Ile Lys Asn
          500

```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

```

Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1          5          10          15
Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
          20          25          30
Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
          35          40

```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

500

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

```

Met Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala
1      5      10      15
Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys
      20      25      30
Asp Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn
      35      40      45
Ile Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr
      50      55      60
Phe Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu
65      70      75      80
Phe Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr
      85      90      95
Ser Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr
      100     105     110
Asn Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr
      115     120     125
Asn Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln
130     135     140
Asn Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr
145     150     155     160
Lys Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser
      165     170     175
Leu Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu
      180     185     190
Ile Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr
195     200     205
Ile Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu
210     215     220
Glu Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile
225     230     235     240
Lys Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr
      245     250     255
Leu Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln
260     265     270
Glu Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln
275     280     285
Ile Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn
290     295     300
Thr Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe
305     310     315     320
Glu Leu Glu Lys Glu Ser Ala Ser Asp Phe Ile Arg His Ser Tyr Ser
      325     330     335
Met Leu Glu Lys Ala
      340

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

501

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

```

Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys Cys Ala Phe Leu
1      5      10      15
Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His Ser Lys Gly Leu
20     25     30
His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro Asn Leu Phe Ser
35     40     45
Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro Val Glu Glu Ser
50     55     60
Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr Val Val Lys Thr
65     70     75     80
Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro Ile Glu Trp Ala
85     90     95
Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp Asn Ser Lys Glu
100    105    110
Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu Ser Ser Arg Val
115    120    125
Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile Thr Lys Arg Tyr
130    135    140
Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu Phe Phe Ile Lys
145    150    155    160
Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys Glu Leu Lys Glu
165    170    175
Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu Thr His Lys Lys
180    185    190
Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr Asp His Leu Lys
195    200    205
Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly Gly Leu Val Arg
210    215    220
Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe Lys Leu Tyr Asn
225    230    235    240
Lys Leu Pro Phe Glu Ser Ile Asn Asn Glu Asn Thr Lys Leu Asn Thr
245    250    255
Asn Asp Asn Glu Glu Val Lys Lys Leu Glu Phe Glu Leu Ala Lys Glu
260    265    270
Val His Ile Leu Ile Leu Glu Gln Gln Leu Leu Ser Ala Thr Asn Tyr
275    280    285
Tyr Ser Trp Ile Asp Lys Asp Asp Asn Ala Asn Phe Ala Trp Lys Met
290    295    300
His Arg Leu Ile Asn Glu Asn Lys Leu Lys Glu Asn His Leu Ser Ala
305    310    315    320
Asn Asn Ala Asn Lys Ile Lys Gln Phe Phe Phe Asn Asn Gly Ser Ile
325    330    335
Leu Gly Trp Thr Lys Glu Glu Gln Ser Ala Ile Gln Glu Asn Arg Asp
340    345    350
Tyr Ser Leu Arg Ser Ala Leu Leu Ser Leu Glu Glu Ile Ala Gln Ala
355    360    365
Lys Ile Glu Leu Gln Lys Tyr Tyr Glu Ser Val Tyr Val Asn Gly Asp
370    375    380
Gly Asn Lys Arg Glu Ile Lys Pro Phe Lys Glu Ile Leu Arg Asp Thr
385    390    395    400
Asn Asn Phe Glu Lys Ala Tyr Lys Glu Arg Tyr Asp Lys Leu Val Ser
405    410    415
Leu Ser Ala Ala Ile Ile Gln Ala Lys Glu Gly Gly Asn Glu Arg Gln
420    425    430

```

SUBSTITUTE SHEET (RULE 26)

502

Asn Ser Ser Ala Asn Asn Asn Asn Pro Ile Lys Asn Thr Ile Glu Thr
 435 440 445
 Asn Thr Ser Asn Asn Ile Ile Gln Asn Asn Asp Asn Ile Ile Ile Gln
 450 455 460
 Ile
 465

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603

Met Ala Leu Glu Val Val Leu Trp Asp Phe Asp Gly Val Ile Phe Asp
 1 5 10 15
 Ser Met His Leu Lys Tyr Glu Gly Phe Lys Ala Leu Phe Gln Lys His
 20 25 30
 Gly Asn Asp Ser Lys Glu Gly Leu Lys Gln Phe Glu Val Tyr His Tyr
 35 40 45
 Gln Ser Gly Gly Ile Ser Arg Asn Glu Lys Ile Gln Tyr Phe Tyr Asn
 50 55 60
 Glu Ile Leu Lys Thr Pro Ile Ala Gln Glu Glu Ile Asp Ala Leu Ala
 65 70 75 80
 Leu Glu Phe Gly Ala Ile Ile Glu Gln Lys Leu Phe Asp Arg Gly His
 85 90 95
 Leu Asn Ser Glu Val Met Ala Phe Ile Asp Lys His Tyr Gln Asn Tyr
 100 105 110
 Ile Phe His Ile Ala Ser Ala Ala Leu His Ser Glu Leu Gln Val Leu
 115 120 125
 Cys Glu Phe Leu Gly Ile Thr Lys Tyr Phe Lys Ser Val Glu Gly Ser
 130 135 140
 Pro Pro Asp Lys Pro Lys Ile Ile Ala Asn Ile Ile Gln Lys Tyr Ala
 145 150 155 160
 Tyr Asp Pro Ser Arg Met Leu Met Ile Ala Ile Ala Ser Met Ile Met
 165 170 175
 Lys Ala Leu Arg Leu Ile Lys Trp Arg Phe Trp Ala Ile Thr Ala Arg
 180 185 190
 Phe

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

503

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604

```

Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1           5           10           15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
20           25           30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
35           40           45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
50           55           60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65           70           75           80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
85           90           95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
100          105          110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Gln Phe Phe Gly Ser Asn Asp
115          120          125
Ala Leu Leu Asn Met Ser Asn Ala Ile Leu Lys Ser Phe
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605

```

Val Lys Cys Leu Leu Ile Lys Lys Ser Leu Leu Phe Ala Leu Lys Pro
1           5           10           15
Leu Pro Asp Leu Lys Thr Thr Thr Pro Ile Leu Ala Pro Met Ser Val
20           25           30
Val Ala Gly Arg Leu Unk Unk His Leu Val Gln His Tyr Leu Leu Ala
35           40           45
Leu Glu His Val Lys Gly Phe Met Gly Lys Gly Val Ile Leu Gly Gly
50           55           60
Leu Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val
65           70           75           80
Val Gly Met Glu Ser Ala Lys Val Leu Unk Gln Met Gly Unk Lys Val
85           90           95
Thr Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr
100          105          110

```

504

His Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile
 115 120 125
 Gln Ala Leu Asn Gly Unk Val Gly Leu Val Gly Ala Val Leu Val Thr
 130 135 140
 Unk Ser Gln Thr Pro Lys Val Unk Leu Arg Arg His Leu Lys Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606

Met Leu Ala Lys Ile Val Phe Ser Ser Leu Val Ala Phe Gly Val Leu
 1 5 10 15
 Ser Ala Asn Val Glu Gln Phe Gly Ser Phe Phe Asn Glu Ile Lys Lys
 20 25 30
 Glu Gln Glu Glu Val Ala Ala Lys Glu Asp Ala Leu Lys Ala Arg Lys
 35 40 45
 Lys Leu Leu Asn Asn Thr His Asp Phe Leu Glu Asp Leu Val Phe Arg
 50 55 60
 Lys Gln Lys Ile Lys Glu Leu Val Asp Tyr Arg Ala Lys Val Leu Leu
 65 70 75 80
 Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys Glu Ala Leu Glu Lys Glu
 85 90 95
 Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser Lys Ala Tyr Gly Asp Leu
 100 105 110
 Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr Lys Lys Leu Leu Pro Asn
 115 120 125
 Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr Phe Thr Gln Glu Asp Lys
 130 135 140
 Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val Lys Thr Ser Ser Ile Phe
 145 150 155 160
 Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys Ala Gln Ala Leu Leu Gln
 165 170 175
 Met Gly Val Phe Ser Leu Asp Glu Glu Gln Asn Lys Lys Ala Ser Arg
 180 185 190
 Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu Glu Tyr Ser Asn Asn Ile
 195 200 205
 Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp Asn Ile Asp Tyr Tyr Leu
 210 215 220
 Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys Ala Lys Asp Ile Ala Gln
 225 230 235 240
 Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser Glu Arg Leu Ala Phe Ser
 245 250 255
 Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr Leu Arg Gly Tyr Glu Ala
 260 265 270
 Phe Ser Asn Leu Leu Lys Asn Val Lys Asp Asp Val Glu Leu Asn Thr
 275 280 285
 Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu Ser Phe Ala Gln Lys Gln

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```

      290              295              300
Lys Leu Cys Leu Leu Val Leu Asp Ser Phe Asn Phe Asp Thr Gln Ser
305              310              315              320
Lys Lys Ser Ile Leu Lys Lys Thr Asn Glu Tyr Asn Ile Phe Val Asp
      325              330              335
Ser Asp Pro Met Met Ser Asp Lys Thr Thr Met Gln Lys Glu His Tyr
      340              345              350
Lys Ile Phe Asn Phe Phe Lys Thr Val Val Ser Ala Tyr Arg Asn Asn
      355              360              365
Val Ala Lys Asn Asn Pro Phe Glu
      370              375

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607

```

Met Asp Phe Val Gly Phe Glu Asp Leu Lys Cys Lys Asp Lys Glu Asn
1      5      10      15
Ser Gln Lys Val Phe Val Ile Arg Asn Asp Lys Leu Gly Asp Phe Ile
      20      25      30
Leu Glu Ile Pro Ala Leu Ile Ala Leu Lys His Ala Phe Leu Glu Lys
      35      40      45
Gly Val Glu Val Tyr Leu Gly Val Val Val Pro Ser Tyr Thr Thr Pro
      50      55      60
Ile Ala Leu Glu Phe Pro Phe Ile Asp Glu Val Ile Ile Glu Asp Asn
      65      70      75      80
His Leu Ala Thr Thr His Lys Asn Arg Ser Ile Asp Ala Leu Ile Phe
      85      90      95
Leu Phe Ser Asn Phe Lys Asn Ala Lys Leu Ala Phe Ser Leu Arg Lys
      100     105     110
Ser Ile Pro Tyr Ile Leu Ala Pro Lys Thr Lys Ile Tyr Ser Trp Leu
      115     120     125
Tyr Gln Lys Arg Val Arg Gln Asn Arg Ser Leu Cys Leu Lys Thr Glu
      130     135     140
Tyr Glu Tyr Asn Leu Asp Leu Ile His Ala Phe Cys Lys Asp Tyr Asp
      145     150     155     160
Leu Pro Asn Ala Gln Leu Lys Lys Ile Ala Trp Lys Leu Lys Asp Lys
      165     170     175
Ser Lys Glu Arg Ser Ile Ile Ala Ser Lys Leu Asn Ala Asn Val Asp
      180     185     190
Leu Leu Trp Ile Gly Val His Met His Ser Gly Gly Ser Ser Pro Val
      195     200     205
Leu Pro Ala Ser His Phe Ile Glu Leu Ile Ala Ile Leu His Glu Lys
      210     215     220
Leu Ser Cys Glu Ile Ile Leu Ile Cys Gly Pro Gly Glu Arg Lys Ala
      225     230     235     240
Thr Glu Glu Leu Leu Lys Glu Val Pro Phe Ala His Leu Tyr Asp Thr
      245     250     255

```

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```

Ser His Ser Leu Val Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val
      260                265                270
Cys Ile Gly Asn Ala Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp
      275                280                285
Asn Gln Ser Ile Gly Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala
      290                295                300
Arg Trp Arg Pro Phe Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn
      305                310                315                320
Gly Ser Asn Asp Met Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys
      325                330                335
Ile Met Gly Phe Ile Thr Lys Asn Leu Ser His His Met Gln Glu Arg
      340                345                350

```

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608

```

Val Gly Val Leu Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly
1      5      10      15
Leu Cys Val Leu Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala
      20      25      30
Tyr Tyr Leu Met Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu
      35      40      45
Ile Lys Asn Arg Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro
      50      55      60
Ile His Gln Thr Cys Gln Ser Thr Gln Phe Leu Ser Pro Cys Val Arg
      65      70      75      80
Leu Val Phe Ser Pro Ile Gly Arg
      85

```

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

```

Met Ser Leu Gly Ala Val Val Ser Ser Leu Leu Cys His Lys Leu Glu
1      5      10      15
Gly Ala Ile Leu Asp Leu Arg Ala Tyr Arg Unk Unk Ala Tyr Tyr His
      20      25      30
Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu Leu Tyr
      35      40      45
Asn Tyr Ile Lys Ala His Ile Unk Leu Asn Leu Leu Trp Thr Ile Arg
      50      55      60
Asn Arg Thr Unk Ser Leu Gly Lys Phe Thr Gln Asn Pro Thr Glu Gln
65      70      75      80
Pro Pro Thr Asn Asn His
      85

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610

```

Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser
1      5      10      15
Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu Asn
      20      25      30
Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys Leu
      35      40      45
Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu
      50      55      60
His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

508

(B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611

```

Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1      5      10      15
Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
20      25      30
Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
35      40      45
Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
50      55      60
Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65      70      75      80
Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
85      90      95
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

```

Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1      5      10      15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
20      25      30
Ile Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu
35      40      45
Asn Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu
50      55      60
Leu Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro
65      70      75      80
Ser Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile
85      90      95
Leu His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg
100     105     110
Arg Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu
115     120     125
Cys Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu
130     135     140
Trp Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly
145     150     155     160
Ser Ala

```

(2) INFORMATION FOR SEQ ID NO:613:

509

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...58
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

```

Val Ile Met Thr Lys Leu Asp Gly Thr Ser Lys Gly Gly Ala Ile Leu
1           5           10           15
Unk Val Leu Tyr Glu Leu Lys Leu Pro Ile Leu Tyr Leu Gly Met Gly
      20           25           30
Glu Lys Glu Asp Asp Leu Ile Ala Phe Asp Glu Glu Arg Phe Ile Glu
      35           40           45
Asp Leu Val Asp Ala Val Phe Val Glu Gln
50           55

```

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614

```

Val Cys Gly Ala His Gly Lys Ser Ser Ile Thr Unk Met Leu Ser Ala
1           5           10           15
Ile Cys Pro Ala Phe Gly Unk Ile Ile Gly Arg His Ser Lys Glu Phe
      20           25           30
Asp Ser Asn Val Unk Glu Ser Ala Asp Met Ser Leu Val Phe Glu Unk
      35           40           45
Asp Glu Ser Asp Ser Ser Phe Phe Ile Phe Gln Pro Phe Leu Arg Asp
50           55           60
Cys Ala
65

```

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids

510

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10           15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
           20           25           30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
           35           40           45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
50           55           60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65           70           75           80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu
           85           90           95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
100          105          110
Unk Leu Gly Pro
115

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10           15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
           20           25           30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
           35           40           45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
50           55           60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65           70           75           80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu

```

511

	85		90		95										
Asp	Ala	Lys	Ile	Ala	Leu	Asp	Leu	Gly	Gln	Lys	Asn	Leu	Ser	Unk	Unk
	100				105								110		
Unk	Leu	Gly	Pro												
	115														

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

Met	Pro	Asp	Asn	Leu	His	Leu	His	Thr	Leu	Leu	Unk	Lys	Phe	Leu	Gln
1			5						10					15	
Gln	Arg	Ser	Phe	Asn	Tyr	Pro	Asn	Pro	Leu	Cys	Ala	Phe	Ile	Leu	Ile
		20					25					30			
Leu	Cys	Asn	Leu	Pro	Phe	Ile	Leu	Ile	Ser	Val	Leu	Phe	Arg	Leu	Asp
		35				40					45				
Ala	Tyr	Ala	Leu	Ile	Val	Ile	Ser	Leu	Val	Phe	Ile	Unk	Cys	Tyr	Leu
	50				55					60					
Ile	Gly	Unk	Ala	Tyr	Leu	Asn	Arg	Gln	Val	Cys	Ala	Leu	Glu	Lys	Arg
65					70				75					80	
Ala	Phe														

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

Met	Pro	Asp	Asn	Leu	His	Leu	His	Thr	Leu	Leu	Unk	Lys	Phe	Leu	Gln
1			5						10					15	
Gln	Arg	Ser	Phe	Asn	Tyr	Pro	Asn	Pro	Leu	Cys	Ala	Phe	Ile	Leu	Ile
		20					25					30			

512

```

Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
   35                               40                               45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
   50                               55                               60
Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
   65                               70                               75                               80
Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617

```

Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Gly Asn Gly Lys Ala
1      5      10      15
Asp Leu Ser Asn Glu Asn Thr Lys Val Arg Gln Thr Lys Thr Asn Leu
   20      25      30
Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu Lys Thr Glu Leu Asn Asn
   35      40      45
Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu Arg Leu Ala Ala Asp Lys
   50      55      60
Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg Lys Pro Asn
   65      70      75

```

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618

```

Met Asp Leu Gln Gln Ile Asp Glu Leu Glu Asn Lys Phe Glu Glu Gln
1      5      10      15
Glu Glu Gln Ala Gln Asp Thr Pro Leu Lys Gln Glu Pro Ser Thr Lys

```

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				20				25				30			
Glu	Val	Lys	Ile	Pro	Lys	Lys	Arg	Gly	Arg	Lys	Lys	Ser	Leu	Leu	Asp
35				40				45							
Glu	Asp	Lys	Lys	Lys	Ser	Phe	Asn	Ile	Ala	Phe	Ser	Pro	Cys	Val	Ile
50				55				60							
Lys	Glu	Leu	Asn	Glu	Phe	Leu	Leu	Glu	Phe	Gly	Ser	Phe	Lys	Glu	Thr
65				70				75				80			
Arg	Ser	Thr	Phe	Ile	Glu	Glu	Ala	Leu	Ile	Arg	His	Leu	Lys	His	Arg
85				90				95							
Lys	Asn	Thr	Gln	Glu	Gln	Lys	Leu	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Gln
100				105				110							
Asn	Lys	Glu	Lys	Gly	Ile	Met	Lys	Thr	Met	Asn	Leu	Asn	Glu	Phe	Phe
115				120				125							
Thr	His	Lys	Ile	Ile	Tyr	Lys	Asp	Thr	Pro	Leu	Lys	Phe	Lys	Asp	Thr
130				135				140							
Leu	Glu	Gln	Glu	Ile	Ser	Gln	Ala	Ser	Leu	Val	Glu	Lys	Leu	Ile	Leu
145				150				155				160			
Ala	Asn	Ile	Leu	Ala	Asn	Met	Val	Phe	Ala	Lys	Ile	Ser	Asn	Glu	Asn
165				170				175							

(2) INFORMATION FOR SEO ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

```
(A) NAME/KEY: misc_feature
(B) LOCATION 1...144
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619

Met	Gly	Cys	Tyr	Gly	Ile	Gly	Ile	Ser	Arg	Leu	Leu	Ser	Val	Ile	Leu
1				5					10					15	
Glu	Gln	Lys	Ser	Asp	Asp	Leu	Asp	Cys	Val	Trp	Thr	Lys	Asn	Thr	Ala
			20					25					30		
Pro	Phe	Asp	Val	Val	Ile	Val	Val	Ser	Asn	Leu	Lys	Asp	Glu	Ala	Gln
		35					40					45			
Lys	Lys	Leu	Ala	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Leu	Gln	Lys	Gly	Val
	50					55					60				
Asp	Ala	Leu	Leu	Asp	Asp	Arg	Asp	Ala	Arg	Phe	Gly	Ala	Lys	Met	Arg
65				70						75					80
Asp	Phe	Glu	Leu	Ile	Gly	Glu	Arg	Leu	Ala	Leu	Ile	Val	Gly	Lys	Gln
				85					90					95	
Thr	Leu	Glu	Ser	Lys	Glu	Phe	Glu	Cys	Ile	Lys	Arg	Ala	Asn	Leu	Glu
			100					105					110		
Lys	Gln	Thr	Ile	Lys	Asp	Ile	Gly	Ile	Arg	Arg	Lys	Asn	Phe	Arg	Asn
		115					120					125			
Val	Ser	Glu	Arg	Ile	Arg	Gly	Gly	Asn	Gly	Lys	Asn	Ser	Asp	Trp	Leu
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

514

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620

```

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1           5           10           15
Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
          20           25           30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
          35           40           45
Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
50           55           60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65           70           75           80
Val Trp Arg Ile Gln Ala Gly Lys Gly Leu
          85           90

```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621

```

Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn
1           5           10           15
Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile
          20           25           30
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val
          35           40           45
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile
50           55           60
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn
65           70           75           80
Met Asp Ser Pro Lys Gln Glu Asp Lys Leu Asp Lys Val Val Asp Asn
          85           90           95
Ile Lys Lys Gln Glu Ser Glu Asn Ser Met Pro Ile Gln Thr Asp Gln
          100          105          110
Ala Gln Met Glu Met Lys Thr Thr Glu Glu Lys Gln Glu Ser Gln Lys

```

515

```

      115              120              125
Glu Leu Lys Ala Val Glu Pro Ile Pro Met Ser Thr Gln Lys Glu Ser
  130              135              140
Gln Ala Val Ala Lys Lys Glu Thr Pro His Lys Lys Pro Lys Val Ala
  145              150              155              160
Pro Lys Asp Lys Glu Ala His Lys Asp Lys Ala Lys His Ala Ala Lys
      165              170              175
Glu Pro Lys Val Lys Lys Glu Ala Arg Lys Glu Val Ser Lys Lys Ala
      180              185              190
Asn Ser Lys Thr Asn Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val
      195              200              205
Phe Ala His Thr Pro Asn Lys Ala Phe Leu Gln Glu Phe Asn Gln Phe
  210              215              220
Pro His Lys Ile Glu Asp Arg Gly Ala Thr Lys Arg Tyr Leu Ile Gly
  225              230              235              240
Pro Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser
      245              250              255
Lys Lys Met Thr Lys Pro Val Val Ile Glu Val Arg
      260              265

```

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622

```

Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe Val Leu Met
 1      5      10      15
Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys Ala Lys His
 20      25      30
Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu Glu Ser Leu
 35      40      45
Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg Gln Met Val
 50      55      60
Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu Leu Leu Asp
 65      70      75      80
Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu Phe Phe Asp
 85      90      95
Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val Leu Val Asn
 100     105     110
Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His Val Val Met
 115     120     125
Leu Lys Asp Lys Lys Leu Phe Leu Gln Ala Ser Thr Pro Ile Ala Met
 130     135     140
Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu Unk Ala Ile
 145     150     155     160
Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
      165      170

```

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(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623

```

Met Met Ala His Ser Leu Ile Leu Val Ser Lys Thr Ser Leu Ser Asn
1           5           10           15
Leu Leu Ile Phe Val Val Gln Pro Asp Gly Lys Leu Ser Met Thr Asp
          20          25          30
Ala Ala Ile Asp Pro Asn Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg
          35          40          45
Val Asn Glu Ile Ala Glu Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu
          50          55          60
Val Thr Val Ile Asn Lys Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn
65          70          75          80
Tyr Asn Ile Lys Asn Tyr Gly Glu Leu Glu Arg Val Ile Lys Lys Leu
          85          90          95
Pro Leu Val Arg Asp Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1           5           10           15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
          20          25          30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
          35          40          45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
50          55          60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp

```

517

```

65          70          75          80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
      85          90          95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
      100         105         110
His Phe Cys Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1          5          10          15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
      20          25          30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
      35          40          45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
      50          55          60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
65          70          75          80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
      85          90          95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
      100         105         110
His Phe Cys Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625

```

Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu Asn
1      5      10      15
Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile Pro
      20      25      30
Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser Ser
      35      40      45
Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr Ile
      50      55      60
Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu Ser
65      70      75      80
Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln Thr
      85      90      95
Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn Ala
      100     105     110
Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile Gly
      115     120     125
Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met Met
      130     135     140
Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala Leu
145     150     155     160
His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser His
      165     170     175
Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala Leu
      180     185     190
Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val Ser
      195     200     205
Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp Leu
      210     215     220
Tyr Tyr His Tyr Leu Lys Ile Val Lys Arg His Phe Val
225     230     235

```

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

```

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1      5      10      15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
      20      25      30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
      35      40      45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
      50      55      60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65      70      75      80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr

```

519

[illegible]

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

[illegible]

520

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627

```

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1          5          10          15
Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
20          25          30
His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
35          40          45
Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
50          55          60
Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65          70          75          80
His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
85          90          95
Val Gly Ile Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
100         105         110
Tyr Phe Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
115         120         125
Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
130         135         140
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145         150         155         160
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
165         170         175
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
180         185         190
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
195         200         205
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
210         215         220
Ile
225

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

521

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
 1           5           10          15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
      20           25           30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
      35           40           45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
      50           55           60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65           70           75           80
Ala Arg Gly His Val
                  85

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
 1           5           10          15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
      20           25           30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
      35           40           45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
      50           55           60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65           70           75           80
Ala Arg Gly His Val
                  85

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

522

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629

```

Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile Ile Ser Phe Phe
 1      5      10      15
Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu Pro Ile Val Ser
      20      25      30
Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu Ile Pro Ser Tyr
      35      40      45
Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr Gly Tyr Thr Ser
      50      55      60
Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln Gly Val Ile Glu
      65      70      75      80
Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala Ser Asn Leu Val
      85      90      95
Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser Ala Trp Ala Ser
      100     105     110
Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro Ser Ser Gly Cys
      115     120     125
Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile Asp Val Ser Met
      130     135     140
Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln Asn Phe Thr Lys
      145     150     155     160
Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu Leu Gln Ile Ile
      165     170     175
Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr Ala Asp Gly Leu
      180     185     190
Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys Leu Gln Asn Asn
      195     200     205
Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser Val Val Lys Gly
      210     215     220
Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val Asn Leu Pro Asp
      225     230     235     240
Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val Ser Tyr Leu Ile
      245     250     255
Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe Met Lys Leu Arg
      260     265     270
Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe Glu Tyr Met Arg
      275     280     285
Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val Ser Phe Ile Ala
      290     295     300
Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr Ser Ile Tyr Phe
      305     310     315     320
Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu Phe Trp Ala Leu
      325     330     335
Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu Pro Ala Val Arg
      340     345     350
Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser Leu Leu Gln Gly
      355     360     365
Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe Met Gln Val Thr
      370     375     380
Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro Leu Ile Ala Gly
      385     390     395     400
Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys Leu Ile Val Leu
      405     410     415
Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile Trp Phe Ile Asn
      420     425     430
Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu Leu Phe Gly Val

```

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	435		440		445		
Leu	Ala	Leu	Leu	Ala	Phe	Asn	Leu
	450				455		460
Gln	Asn	Ile	Asn	Gln	Gly	Gly	Ile
465				470		475	480
Leu	Ile	Thr	Leu	Phe	Ile	Leu	Lys
			485			490	
							495

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630

Met	Ala	Phe	Trp	Gln	Ala	Ile	Arg	Trp	Trp	Ile	Leu	Lys	Leu	Pro	Phe
1				5					10					15	
Met	Met	Gly	Ala	Thr	Met	Met	Trp	Ile	Leu	Ser	Glu	Met	Ala	Phe	Lys
		20					25						30		
Ile	Ala	Gly	Unk	Met	Ala	Phe	Lys	Glu	Ala	Ser	Arg	Ala	Ala	Asn	Pro
		35				40					45				
Val	Leu	Leu	Glu	Pro	Met	Met	Lys	Val	Glu	Val	Glu	Val	Pro	Glu	Glu
	50				55				60						
Tyr	Met	Gly	Asp	Val	Ile	Gly	Asp	Leu	Asn	Arg	Arg	Arg	Gly	Gln	Ile
65				70				75						80	
Asn	Ser	Met	Asp	Asp	Arg	Leu	Gly	Leu	Lys	Ile	Val	Asn	Ala	Phe	Val
			85					90					95		
Pro	Leu	Val	Glu	Met	Phe	Gly	Tyr	Ser	Thr	Asp	Leu	Arg	Ser	Ala	Thr
		100					105					110			
Gln	Gly	Arg	Gly	Thr	Tyr	Ser	Met	Glu	Phe	Asp	His	Tyr	Gly	Glu	Val
	115					120					125				
Pro	Ser	Asn	Ile	Ala	Lys	Glu	Ile	Val	Glu	Lys	Arg	Lys	Gly		
	130				135						140				

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631

```

Met Gln Asn Leu Pro Gly Met Ala Arg Ala Ala Met Leu Thr Thr Ser
1      5      10      15
Ser Ala Pro Ala Pro Glu Gly Glu Gly Ala Phe Arg Ala Met Lys Met
20      25      30
Ala Ser Glu Met Ala Lys Val Glu Val Gly Tyr Val Asn Ala His Gly
35      40      45
Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile Ala Leu Lys Asn
50      55      60
Val Leu Ala Leu Lys Lys Lys Ser Leu Leu Leu Ala Pro Leu Lys Gly
65      70      75      80
Arg Leu Gly Leu Leu Gly Cys Cys Gly Val Arg Ser Arg Tyr Ser Ile
85      90      95
Met Ala Met Unk Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Thr
100     105     110
Pro Asp Pro Glu Cys Unk Leu Asp Tyr Ile Pro Asn Thr Ala Arg Glu
115     120     125
Lys Gln Val Asn Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr
130     135     140
Asn Gly Val Val Ile Phe Lys Lys Ala
145     150

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

```

Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1      5      10      15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
20      25      30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
35      40      45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
50      55      60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65      70      75      80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
85      90      95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
100     105     110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
115     120     125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
130     135     140
Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro

```

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```

145          150          155          160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
          165          170          175
Lys Arg Arg Tyr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
          180          185          190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
          195          200          205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
          210          215          220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225          230          235          240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
          245          250          255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
          260          265          270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
          275          280          285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
          290          295          300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305          310          315          320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
          325          330          335
Phe Tyr Asp Phe Leu Val Phe
          340

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

```

Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1          5          10          15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
          20          25          30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
          35          40          45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
          50          55          60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65          70          75          80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
          85          90          95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
          100          105          110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
          115          120          125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
130          135          140

```

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```

Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro
145          150          155          160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
          165          170          175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
          180          185          190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
          195          200          205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
          210          215          220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225          230          235          240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
          245          250          255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
          260          265          270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
          275          280          285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
290          295          300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305          310          315          320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
          325          330          335
Phe Tyr Asp Phe Leu Val Phe
          340

```

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633

```

Met Ile Leu Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu
1           5           10           15
Ile Phe Ile Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn
          20           25           30
Glu Val Ala Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe
          35           40           45
Pro Asn Tyr Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp
          50           55           60
Ala Lys Ser Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn
65           70           75           80
Leu Ser Tyr Val Asn Asp Phe Ile Ser Lys Val Gln Lys
          85           90

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

```

Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1      5      10      15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
      20      25      30
Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
      35      40      45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
      50      55      60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
      65      70      75      80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
      85      90      95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
      100     105     110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
      115     120     125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
      130     135     140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
      145     150     155     160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
      165     170     175

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

```

Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1      5      10      15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
      20      25      30

```

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```

Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
   35           40           45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
   50           55           60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
   65           70           75           80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
           85           90           95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
           100          105          110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
           115          120          125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
           130          135          140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
           145          150          155          160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
           165          170          175

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635

```

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
  1           5           10           15
Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
           20           25           30
Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
           35           40           45
Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
           50           55           60
Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
           65           70           75           80
Lys Leu Ile Pro Lys Ile Ile Gly
           85

```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636

```

Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1      5      10      15
Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
      20      25      30
Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
      35      40      45
Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
      50      55      60
Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
65      70      75      80
Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
      85      90      95
Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
      100      105      110
Gly Ala Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1      5      10      15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
      20      25      30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
      35      40      45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
      50      55      60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65      70      75      80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
      85      90      95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
      100      105      110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
      115      120      125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
      130      135      140

```

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```

Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145          150          155          160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
          165          170          175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
          180          185          190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
          195          200          205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr
          210          215          220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
225          230          235          240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
          245          250          255
Ala Lys Lys Asn
          260

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1          5          10          15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
          20          25          30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
          35          40          45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
          50          55          60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65          70          75          80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
          85          90          95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
          100          105          110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
          115          120          125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
          130          135          140
Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145          150          155          160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
          165          170          175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
          180          185          190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
          195          200          205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr

```

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```

      210                215                220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
225                230                235                240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
      245                250                255
Ala Lys Lys Asn
      260

```

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638

```

Met Lys Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val
1          5          10          15
Ala Asp Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro
      20          25          30
Arg Glu Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile
      35          40          45
Ile Arg Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe
      50          55          60
Gly Ser Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp
      65          70          75          80
Pro Lys Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu
      85          90          95
Leu Arg Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp
      100         105         110
Ile Gly Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala
      115         120         125
Lys Asn Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe
      130         135         140
Ile Ile Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu
      145         150         155         160
Glu Met Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile
      165         170         175
Thr Gln Asp Tyr Ala Met Ile Arg Asn Thr Ile Ala Met Met Ile
      180         185         190

```

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639

```

Met Ile Ser Glu Ile Ile Lys Phe Gln Leu Lys Gly Ile Lys Met Ile
1      5      10      15
Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys Thr Ser Leu Leu Ala Gly
20      25      30
Val Leu Leu Gly Ala Thr Ala Pro Leu Met Ala Lys Pro Leu Leu Ser
35      40      45
Asp Glu Asp Leu Leu Lys Arg Val Lys Leu His Asn Ile Lys Glu Asp
50      55      60
Thr Leu Thr Ser Cys Asn Ala Lys Val Asp Gly Ser Gln Tyr Leu Asn
65      70      75      80
Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro Gln Glu Tyr Arg Glu Lys
85      90      95
Ile Phe Glu Cys Val Glu Glu Glu Lys His Lys Gln Ala Leu Asn Leu
100     105     110
Ile Asn Lys Glu Asp Thr Glu Asp Lys Glu Glu Leu Ala Lys Lys Ile
115     120     125
Lys Glu Ile Lys Glu Lys Ala Lys Val Leu Arg Gln Lys Phe Met Ala
130     135     140
Phe Glu Met Lys Glu His Ser Lys Glu Phe Pro Asn Lys Lys Gln Leu
145     150     155     160
Gln Thr Met Leu Glu Asn Ala Phe Asp Asn Gly Ala Glu Ser Phe Ile
165     170     175
Asp Asp Trp His Glu Arg Phe Gly Gly Ile Ser Arg Glu Asn Thr Tyr
180     185     190
Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp Glu Gly Lys Ile Leu Ala
195     200     205
Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr Lys Lys Asp Phe Glu Glu
210     215     220
Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser Ala Met Ala Asn Met Ser
225     230     235     240
Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu Lys Pro Lys Tyr Gln Leu
245     250     255
His Ser Ser Asn Asn Ile Lys Pro Leu Met Ser Asn Thr Glu Leu Leu
260     265     270
Asn Met Ile Glu Leu Thr Asn Ile Lys Lys Glu Tyr Val Met Gly Cys
275     280     285
Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro Ile His Lys Asp Trp Gly
290     295     300
Phe Phe Gly Lys Ala Lys Val Pro Glu Thr Trp Arg Asn Lys Ile Trp
305     310     315     320
Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr Asp Asn Thr Thr Ala Glu
325     330     335
Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr Ser Ile Ser His His
340     345     350

```

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

533

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640

```

Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu Val
1      5      10      15
Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile Ile
20      25      30
Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg Val
35      40      45
Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met Ala
50      55      60
Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val Glu
65      70      75      80
Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu Met
85      90      95
Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro Met
100     105     110
Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro Met
115     120     125
Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn Arg
130     135     140
Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg Gln
145     150     155     160
Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met Tyr
165     170     175
Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile Val
180     185     190
Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile Gly
195     200     205
His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile Glu
210     215     220
Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu Thr
225     230     235     240
Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser Gly
245     250     255
Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser Leu
260     265     270
Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn Lys
275     280     285
Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Arg Tyr
290     295     300
Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile Lys
305     310     315     320
Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu Met
325     330     335
Leu Glu Glu Gln Arg Arg Arg Gln Ser Trp Ala Met Leu Trp Ser
340     345     350

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```

Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1           5           10           15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
          20           25           30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
          35           40           45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
          50           55           60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
          65           70           75           80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
          85           90           95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
          100          105          110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
          115          120          125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
          130          135          140
Gly
145

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```

Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1           5           10           15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
          20           25           30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
          35           40           45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
          50           55           60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
          65           70           75           80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro

```

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```

      85          90          95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
      100      105      110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
      115      120      125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
      130      135      140
Gly
145

```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642

```

Met Pro Thr Met Leu Ala Val Gly Phe Trp Val Leu Val Phe Leu Ser
1          5          10          15
Thr Ser Asn Ala Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser
      20      25      30
Val Pro Ser Ile Phe Thr Leu Leu Ser Leu Ser Ile Phe Val Tyr Val
      35      40      45
Ala Gly Asn Ala Glu Phe Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile
50      55      60
Asp Val Gly Glu Leu Phe Val Ile Ser Leu Ala Leu Val Gly Ser Leu
65      70      75      80
Phe Gly Phe Leu Trp Tyr Asn Cys Asn Pro Ala Ser Val Phe Met Gly
      85      90      95
Asp Ser Gly Ser Leu Ala Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile
      100      105      110
Val Ser His Asn Glu Ile Leu Leu Val Leu Met Gly Ser Ile Phe Val
      115      120      125
Ile Glu Thr Leu Ser Val Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg
130      135      140
Lys Lys Arg Leu Phe Leu Met Ala Pro Ile His His His Phe Glu Gln
145      150      155      160
Lys Gly Trp Ala Glu Asn Lys Val Ile Val Arg Phe Trp Ile Ile Ser
      165      170      175
Met Leu Ser Asn Leu Val Ala Leu Leu Ser Leu Lys Val Cys
      180      185      190

```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643

```

Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala Thr
1      5      10      15
Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu Ser
20      25      30
Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe Phe
35      40      45
Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu Lys
50      55      60
Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn Leu
65      70      75      80
Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser Leu
85      90      95
Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser Asp
100     105     110
Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp Asn
115     120     125
Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys Thr
130     135     140
Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly Phe
145     150     155     160
Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Glu Ser Asp Leu Ile Thr
165     170     175
Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr Gly
180     185     190
Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys Glu
195     200     205
Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys Ala
210     215     220
Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr Phe
225     230     235     240
His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu Asn
245     250     255
Ser Asp Ala Unk Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu Asn
260     265     270
Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu Glu
275     280     285
Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu Lys
290     295     300
Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp Phe
305     310     315     320
Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile Glu
325     330     335
Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu Asn
340     345     350
Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr Glu
355     360     365
Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn Leu
370     375     380
Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser Ile
385     390     395     400
Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser Thr
405     410     415
Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Asp Ala

```

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```

          420          425          430
Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu Ser
          435          440          445
Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu Ala
          450          455          460
Ile Lys Glu Gln Ala Glu Thr Lys Arg Cys Asn Ala Gly Asn Ala Phe
          465          470          475          480
Cys Asp Thr Tyr Gln Pro Cys Lys Pro
          485

```

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1          5          10          15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
          20          25          30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
          35          40          45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
          50          55          60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
          65          70          75          80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
          85          90          95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
          100          105          110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
          115          120          125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
          130          135          140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
          145          150          155          160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
          165          170          175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
          180          185          190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
          195          200          205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
          210          215          220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
          225          230          235          240
Val Phe Leu Ser Gly Val Lys Asn
          245

```

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(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1           5           10           15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
          20           25           30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
          35           40           45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
          50           55           60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65           70           75           80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
          85           90           95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
          100          105          110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
          115          120          125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
          130          135          140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145          150          155          160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
          165          170          175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
          180          185          190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
          195          200          205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
          210          215          220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225          230          235          240
Val Phe Leu Ser Gly Val Lys Asn
          245

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

539

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1           5           10           15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
20          25          30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
35          40          45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
50          55          60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65          70          75          80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
85          90          95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
100         105         110
Leu Leu Trp Trp Phe Unk Leu
115

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1           5           10           15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
20          25          30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
35          40          45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
50          55          60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65          70          75          80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
85          90          95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
100         105         110
Leu Leu Trp Trp Phe Unk Leu
115

```

540

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

```

Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1           5           10           15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
          20          25          30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
          35          40          45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
          50          55          60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser
65          70          75          80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
          85          90          95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
          100          105

```

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

```

Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1           5           10           15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
          20          25          30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
          35          40          45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
          50          55          60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser

```

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```

65          70          75          80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
          85          90          95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
          100         105

```

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647

```

Val Phe Lys Asn Ser Leu Phe Gly Ile Ser Ile Ser Met Leu Ile Thr
1          5          10          15
Trp Val Leu Thr Ala Cys Ile Leu Ile Phe Ile Leu Phe Val Pro Asn
          20          25          30
Phe Thr Leu Thr His Pro Asn Phe His Phe Thr Pro Phe Glu Lys Thr
          35          40          45
Tyr Phe Gln Ile Leu Gly Leu Val Gly Ile Val Ser Ile Ile Phe
          50          55          60
Thr Gly Phe Leu Ala Asp Lys Ile Lys Pro His Lys Val Cys Met Ala
65          70          75          80
Phe Ser Thr Thr Phe Gly Phe Phe Gly Phe Leu Phe Phe Lys Glu Phe
          85          90          95
Tyr Ser Asn Ala Pro Ser Leu Val Asn Thr Ile Ile Leu Tyr Phe Leu
          100         105         110
Ala Cys Phe Cys Ala Gly Ile Met Asn Phe Cys Pro Ile Phe Met Ser
          115         120         125
Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr
          130         135         140
Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser
145          150         155         160
Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr
          165         170         175
Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr
          180         185         190
Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu
          195         200         205
Val Ser Pro Thr Ala
210

```

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```

Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1          5          10          15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
20          25          30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
35          40          45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
50          55          60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65          70          75          80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
85          90          95
Tyr Leu Gln Glu Lys Unk Unk Ile Phe Pro Thr Unk Lys Unk Unk
100         105         110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
115         120         125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
130         135         140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```

Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1          5          10          15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
20          25          30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
35          40          45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
50          55          60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65          70          75          80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala

```

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				85				90					95		
Tyr	Leu	Gln	Glu	Lys	Unk	Unk	Ile	Phe	Pro	Thr	Unk	Lys	Unk	Unk	Unk
			100					105					110		
Ser	Lys	Ile	Met	Arg	Leu	Asp	Gly	Val	Lys	His	Val	Glu	Lys	Asn	Leu
			115				120					125			
Lys	Asp	Asn	Leu	Glu	Glu	Met	Ser	Asp	Glu	Val	Lys	Asn	Lys	Gly	Ser
			130			135					140				
Ile	Asp	Asn	Ala	Lys	Glu	Ser	Phe	Asn	Lys	Gly	Tyr	Gly			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649

Met 1	Lys	Ser	Asp	Lys 5	Pro	Phe	Leu	Glu	Arg 10	Tyr	Phe	Tyr	Asp	Pro 15	Thr
Leu	Leu	Gln	Lys 20	Gly	Leu	Ile	Phe	Ala 25	Leu	Tyr	Pro	Phe	Ser 30	Leu	Ile
Tyr	Gln 35	Cys	Ile	Ala	Thr	Ile	Lys 40	Arg	Lys	Thr	Ala	Lys 45	Lys	His	Asp
Phe	Lys 50	Ile	Pro	Ile	Ile	Ser 55	Ile	Gly	Asn	Leu	Ile 60	Ala	Gly	Gly	Ser
Gly 65	Lys	Thr	Pro	Phe	Ile 70	Leu	Glu	Ile	Ala 75	Pro	Arg	Tyr	Gln	Glu	Val 80
Ala	Val	Val	Ser 85	Arg	Gly	Tyr	Gln	Arg	Asp 90	Ser	Lys	Gly	Leu 95	Val	Val
Val	Ser	Val	Lys 100	Gly	Asn	Ile	Leu	Val 105	Pro	Gln	Lys	Thr	Ala 110	Gly	Asp
Glu	Ala	Tyr 115	Leu	Leu	Ala	Leu	Asn 120	Leu	Lys	Gln	Ala	Ser 125	Val	Ile	Val
Ser	Glu 130	Lys	Arg	Glu	Leu	Gly 135	Val	Leu	Lys	Ala	Leu 140	Glu	Leu	Gly	Ser
Lys 145	Ile	Val	Phe	Leu	Asp 150	Asp	Gly	Phe	Arg	Phe 155	Asn	Phe	Asn	Gln	Phe 160
Asn	Ala	Leu	Leu 165	Lys	Pro	Lys	Val	Pro	Pro 170	Tyr	Tyr	Pro	Phe 175	Cys	Leu
Pro	Ser	Gly 180	Leu	Tyr	Arg	Glu	Asn 185	Ile	Lys	Ser	Tyr	Lys	Glu 190	Ala	His
Leu	Val 195	Ile	Thr	Glu	Asp	Lys	Asp 200	Tyr	Gln	Arg	Ile 205	Thr	Ser	Ile	Thr
Asn	Pro 210	Thr	Lys	Arg	Met	Leu 215	Leu	Val	Thr	Ala	Ile 220	Ala	Asn	Pro	Ser
Arg 225	Leu	Asp	Ala	Phe	Leu 230	Pro	Lys	Glu	Val	Val 235	Lys	Lys	Leu	Tyr	Phe 240
Arg	Asp	His	Ala 245	Pro	Phe	Asp	Leu	Lys 250	Leu	Leu	Glu	Lys	Glu 255	Phe	Tyr
Gln	Asn	Asn	Ala 260	Thr	Ser	Leu	Leu 265	Val	Thr	Ser	Lys	Asp	Leu 270	Val	Lys

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Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
 275 280 285
 Ile Cys Pro Lys Val Leu Glu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
 290 295 300
 Pro Cys Asn Ile Lys Glu His Leu
 305 310

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...56

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650

Met Ser Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu
 1 5 10 15
 Gly Val Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro
 20 25 30
 Asn Asn Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser
 35 40 45
 Ser Thr Ser Lys Phe Ile Leu Leu
 50 55

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651

Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys Ile
 1 5 10 15
 Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile Ser
 20 25 30
 Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala Pro
 35 40 45
 Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile Cys

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50		55		60
Asp	Lys	Gly	Glu	Trp
65		70		75
Ile	Phe	Asn	Tyr	Phe
		85		90
Gly	Gln	Leu	Pro	Gly
		100		105
Met	Lys	Glu	Phe	Glu
		115		120
Gly	Glu	Trp	Leu	Glu
		130		135
Gly	Phe	Asn	Gly	Val
145		150		155
Phe	Arg	Glu	Gly	Val
		165		170
Pro	Lys	Leu	Pro	Asn
		180		185
Tyr	Ala	Gly	Arg	Leu
		195		

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

Leu	Ser	Lys	Gln	Ser	Ala	Asp	Ile	Val	Ile	Thr	Asn	Asp	Ser	Leu	Ser
1			5					10						15	
Ser	Leu	Val	Lys	Val	Leu	Ala	Ile	Ala	Lys	Lys	Thr	Lys	Ser	Ile	Thr
		20					25					30			
Trp	Gln	Asn	Ile	Leu	Phe	Ala	Leu	Gly	Ile	Lys	Ala	Val	Phe	Ile	Val
		35					40					45			
Leu	Gly	Leu	Met	Gly	Val	Ala	Ser	Leu	Trp	Glu	Ala	Val	Phe	Gly	Asp
		50				55				60					
Val	Gly	Val	Thr	Leu	Leu	Ala	Leu	Ala	Asn	Ser	Unk	Arg	Thr	Met	Arg
65				70					75					80	
Ala															

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

546

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

```

Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1           5           10           15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
          20           25           30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
          35           40           45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
50           55           60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Unk Arg Thr Met Arg
65           70           75           80
Ala

```

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653

```

Met Leu Lys Asn Gly Asp Lys Ile Pro Asp Ala Ile Leu Val Asp Ile
1           5           10           15
Glu Met Pro Lys Met Asp Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys
          20           25           30
Tyr Asn Lys Phe Lys Asn Leu Pro Leu Ile Ala Val Thr Ser Arg Val
          35           40           45
Thr Lys Thr Asp Arg Met Arg Gly Val Glu Ser Gly Met Thr Glu Tyr
50           55           60
Ile Thr Lys Pro Tyr Ser Gly Glu Tyr Leu Thr Thr Val Val Lys Arg
65           70           75           80
Ser Ile Lys Leu Glu Gly Asp Gln Ser
          85

```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

547

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654

```

Val Phe Glu Pro Val Ile Ala Tyr Lys Leu Phe His Ser Phe Val Ile
1           5           10           15
Leu Gly Cys Ala Ile Glu Thr Leu Thr Thr Lys Cys Val Glu Gly Ile
          20           25           30
Thr Ala Asn Glu Lys Ile Cys His Asp Tyr Val Phe Asn Ser Ile Gly
          35           40           45
Ile Val Thr Ala Leu Asn Pro His Ile Gly Tyr Glu Lys Ser Ala Met
          50           55           60
Ile Ala Lys Glu Ala Leu Lys Ser Asp Arg Ser Ile Tyr Asp Ile Ala
65           70           75           80
Leu Glu Lys Lys Ile Leu Thr Lys Glu Gln Leu Asp Asp Ile Phe Lys
          85           90           95
Pro Glu Asn Met Leu Arg Thr His Ala Phe Lys Lys His Lys Asp
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655

```

Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1           5           10           15
Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
          20           25           30
Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
          35           40           45
Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
50           55           60
Gln
65

```

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

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548

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656

```

Met Lys Lys Leu Leu Leu Leu Glu His Lys Ile Val Lys Ile Gly
1      5      10      15
Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu Phe Tyr Glu Gln
      20      25      30
Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly Lys Phe Pro Thr
      35      40      45
Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys Asn Lys Ile Asp
50      55      60
Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys Ser Val Asn Glu
65      70      75      80
Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe Asn Ala Leu Val
      85      90      95
Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys Thr Leu Ile Lys
      100     105     110
Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn Glu Asp Glu Lys
      115     120     125
Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser Gln Lys Glu Thr
130     135     140
Gln Pro Pro Ile Ser Ile Lys Asn Ser Val Ser His Ile Lys Ser Lys
145     150     155     160
Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro Ser Val Ser Phe
      165     170     175
Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Ser Phe Ser Ser Phe Glu
      180     185     190
Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys Glu Lys Leu Lys
      195     200     205
Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser Leu Leu Ser Ser
210     215     220
Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu Ile Gly Leu Ile
225     230     235     240
Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn Ala Ser Asn Asn
      245     250     255
Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
      260     265

```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

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549

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657

```

Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser
1           5           10           15
Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu
20           25           30
Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys
35           40           45
Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu
50           55           60
Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys
65           70           75           80
Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn
85           90           95
Leu Lys Gln Gly
100

```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658

```

Val Met Asp Lys Leu Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala
1           5           10           15
Tyr Leu Gly Lys Ile Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn
20           25           30
Glu His Pro Gln Thr Ile Ala Leu Ile Leu Ala His Met Glu Unk Pro
35           40           45
Asn Ala Ala Glu Thr Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu
50           55           60
Ile Ser Ile Arg Met Ala Asn Phe Arg Arg Asn Ile Ala Pro Ser Gly
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

550

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659

```

Met Arg Tyr Phe Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe
1          5          10          15
Phe Val Ser Cys Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr
20          25          30
Lys Glu Arg Ile Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr
35          40          45
Leu Asn Ala Leu Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val
50          55          60
Phe Arg Phe Tyr Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn
65          70          75          80
Thr Glu Val Thr Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr
85          90          95
Met Thr Lys Arg Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp
100          105          110
Ile Ala Ala Arg Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe
115          120          125
Asp Asp Ile Val Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg
130          135          140
His Leu Thr Pro Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu
145          150          155          160
Ile Ile Leu Tyr Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu
165          170          175
Thr Gln Lys Ile Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln
180          185          190
Asp Leu Glu Asp Asn Glu Asn Ala Asp Ser Glu Leu Gln
195          200          205

```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660

```

Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
1          5          10          15
Val Val Glu Pro Val Ala Arg Ile Gly Ile Unk Ala Phe Thr Asn Asp
20          25          30
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
35          40          45
Thr Ile Asn Gly Glu Asn Arg Pro Leu Unk Gly Asn Pro Ile Leu Gly

```

551

50	55	60
Trp Asp Glu Glu Gly Lys Leu Lys Phe Gly Lys Ile Arg His Lys Tyr		
65	70	75
Leu Glu Thr Ser Asn Val Asn Ala Gly Asn Ala Leu Thr Asn Leu Ile		80
	85	90
Leu Met Gln Arg Gly Tyr Ser Met Asn Ala Arg Ala Phe Gly Ala Gly		95
	100	105
Asp Asp Met Ile Lys Glu Ala Ile Ser Leu Lys Lys		110
115	120	

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661

Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His	
1	5
Val Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala	
	20
Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr	
	35
Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val	
	50
Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala	
65	70
Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe	
	85

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

552

```

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1           5           10           15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
          20           25           30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
          35           40           45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
          50           55           60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

```

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1           5           10           15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
          20           25           30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
          35           40           45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
          50           55           60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663

Val Glu Glu Leu Ala Lys Leu Ile Asn Asn Asn Asn Asn Asn Lys Lys

553

```

1           5           10           15
Leu Arg Gly Phe Phe Leu Lys Val Leu Leu Ser Leu Val Val Phe Ser
                20           25           30
Ser Tyr Gly Ser Ala Asn Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu
                35           40           45
Glu Lys Glu Lys Asn Thr Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp
                50           55           60
Phe Asp Ser Phe Lys Ala Thr Ile Lys Asn Leu Lys Asp Lys Lys Val
65           70           75           80
Thr Phe Lys Glu Val Asn Pro Asp Ile Ile Lys Asp Glu Val Phe Asp
                85           90           95
Phe Val Ile Val Asn Arg Val Leu Lys Lys Ile Lys Asp Leu Lys His
                100           105           110
Tyr Asp Pro Val Ile Glu Lys Ile Phe Asp Glu Lys Gly Lys Glu Met
                115           120           125
Gly Leu Asn Val Glu Leu Gln Ile Asn Pro Glu Val Lys Asp Phe Phe
130           135           140
Thr Phe Lys Ser Ile Ser Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser
145           150           155           160
Leu His Gly Glu Thr Arg Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn
                165           170           175
Val Leu Leu Ala Val Phe Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys
                180           185           190
His Ile Ser Thr Ile Glu Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr
                195           200           205
Cys Glu Ala Val Tyr Leu
210

```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664

```

Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser Thr Tyr Met Val
1           5           10           15
Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser Ala Leu Asp Leu
                20           25           30
Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys Ala Tyr Pro Lys
                35           40           45
Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu Asn Gly Ser Leu
50           55           60
Glu Pro Thr Asn Glu Gly Tyr Ala Leu Pro Asn Ser Leu Unk
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

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554

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665

```

Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe Asn Val Ile Ile
1      5      10      15
Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile His Lys Thr Leu
20     25     30
Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly Lys Leu Gly Ile
35     40     45
Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser Leu Glu Val Glu
50     55     60
Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro Thr Lys Lys Arg
65     70     75     80
Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr Gly Ile Trp Ala
85     90     95
Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile Ile Leu Asp Asp
100    105    110
Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys Tyr Glu Unk Arg
115    120    125
Ile Ser Arg Asn Gln Arg Gly Ile Phe Pro Arg Arg Leu Lys Ile
130    135    140
Ser Ser Leu Lys Ser Ser Ile Cys Phe Leu Lys Met Leu Lys Ser Lys
145    150    155    160
Trp Met Ala Thr Pro Thr Ile Unk Pro Lys Pro Gly Lys Trp Arg Ser
165    170    175
Ile

```

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666

```

Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1      5      10      15
Trp Gly Arg Cys Val Tyr Ala Gly Gly Leu Met Ala Glu Gln Asp Pro

```

[illegible]

Val 1	Ala	Leu	Thr	Leu 5	Gly	Ala	Arg	Gly 10	Gly	Val	Tyr	Leu	Cys	Gly 15	Gly
Ile	Ile	Pro	Arg 20	Phe	Ile	Asp	Tyr	Phe 25	Lys	Thr	Ser	Pro	Phe 30	Arg	Ala
Arg	Phe	Glu 35	Thr	Lys	Gly	Arg	Met 40	Gly	Ala	Phe	Leu	Ala 45	Ser	Ile	Pro
Val	His 50	Val	Val	Met	Lys	Lys 55	Thr	Pro	Gly	Leu	Asp 60	Gly	Ala	Gly	Ile
Ala 65	Leu	Glu	Asn	Tyr	Leu 70	Leu	His	Asp	Arg	Ile 75					

556

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668

```

Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
1      5      10      15
Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
20     25     30
Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
35     40     45
Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
50     55     60
Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
65     70     75     80
Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
85     90     95
Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
100    105    110
Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
115    120    125
Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
130    135    140
Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
145    150    155    160
Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
165    170    175
Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
180    185    190
Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
195    200    205
Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
210    215    220
Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Lys Val Asn Asp
225    230    235    240
Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
245    250    255
Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
260    265    270
Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
275    280    285
Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
290    295    300
Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Ile Lys Ala Ser Asn
305    310    315    320
Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
325    330    335
Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
340    345    350
Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr

```

557

```

          355          360          365
Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
  370          375          380
Glu Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
  385          390          395          400
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
          405          410          415
Phe Ser Ile Trp Asp
          420

```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669

```

Met Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala
 1          5          10          15
Val Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu
 20          25          30
Val Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys
 35          40          45
Ala Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val
 50          55          60
Asn Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe
 65          70          75          80
Ile

```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670

558

```

Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr Phe
1      5      10      15
Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu Ile
      20      25      30
Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met Ser
      35      40      45
Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr Ser
      50      55      60
Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu Arg
      65      70      75      80
Pro Lys Arg Phe Gly Phe Lys Ile Ala Phe Phe Asp Arg Ser Arg His
      85      90      95
Gln His Val Phe Ile Leu Pro His Arg Ala Lys Asp Phe Lys Lys Ala
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

```

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1      5      10      15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
      20      25      30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
      35      40      45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
      50      55      60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
      65      70      75      80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
      85      90      95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
      100      105      110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
      115      120      125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
      130      135      140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
      145      150      155      160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
      165      170      175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
      180      185      190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
      195      200      205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
      210      215      220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr

```

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```

225          230          235          240
Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
          245          250          255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
          260          265          270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
          275          280          285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
          290          295          300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305          310          315          320
Thr Phe Thr Phe Asn
          325

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

```

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1          5          10          15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
          20          25          30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
          35          40          45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
          50          55          60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65          70          75          80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
          85          90          95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
          100          105          110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
          115          120          125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
          130          135          140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145          150          155          160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
          165          170          175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
          180          185          190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
          195          200          205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
          210          215          220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr
225          230          235          240

```

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```

Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
      245      250      255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
      260      265      270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
      275      280      285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
      290      295      300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305      310      315      320
Thr Phe Thr Phe Asn
      325

```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

```

Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser
1      5      10      15
Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser
      20      25      30
Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala
      35      40      45
Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn
      50      55      60
Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly
      65      70      75      80
Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys
      85      90      95
Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe
      100      105      110
Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn
      115      120      125
Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu
      130      135      140
Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile
      145      150      155      160
Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser
      165      170      175
Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly
      180      185      190
Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly
      195      200      205
Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg
      210      215      220
Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr
      225      230      235      240
Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile

```


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			245			250			255
Gln	Thr	Ala	Asp	Ala	Met	Leu	Gln	Thr	Val
			260				265		
								Leu	Lys
									270
									Arg

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

Leu	Leu	Ser	Leu	Val	Lys	Gly	Lys	Thr	Met	Leu	Arg	Ser	Leu	Tyr	Ser
1				5					10					15	
Ala	Thr	Ser	Gly	Met	Leu	Ala	Gln	Gln	Thr	His	Ile	Asp	Thr	Thr	Ser
			20					25					30		
Asn	Asn	Ile	Ala	Asn	Val	Asn	Thr	Thr	Gly	Phe	Lys	Lys	Ser	Arg	Ala
		35					40					45			
Asp	Phe	Asn	Asp	Leu	Phe	Tyr	Gln	Ala	Met	Gln	Tyr	Ala	Gly	Thr	Asn
50						55					60				
Thr	Ser	Asn	Thr	Thr	Leu	Ser	Pro	Asp	Gly	Met	Glu	Val	Gly	Leu	Gly
65					70					75				80	
Val	Arg	Pro	Ser	Ala	Ile	Thr	Lys	Met	Phe	Ser	Gln	Gly	Ser	Pro	Lys
				85					90					95	
Glu	Thr	Glu	Asn	Asn	Leu	Asp	Ile	Ala	Ile	Thr	Gly	Lys	Gly	Phe	Phe
			100					105					110		
Gln	Val	Gln	Leu	Pro	Asp	Gly	Thr	Thr	Ala	Tyr	Thr	Arg	Ser	Gly	Asn
		115					120					125			
Phe	Lys	Leu	Asp	Glu	Gln	Gly	Asn	Leu	Val	Thr	Ser	Glu	Gly	Tyr	Leu
130						135					140				
Leu	Ile	Pro	Gln	Ile	Thr	Leu	Pro	Glu	Asp	Thr	Thr	Gln	Val	Asn	Ile
145				150					155					160	
Gly	Val	Asp	Gly	Thr	Val	Ser	Val	Thr	Gln	Gly	Leu	Gln	Thr	Thr	Ser
			165						170					175	
Asn	Val	Ile	Gly	Gln	Ile	Thr	Leu	Ala	Asn	Phe	Val	Asn	Pro	Ala	Gly
			180					185					190		
Leu	His	Ser	Met	Gly	Asp	Asn	Leu	Phe	Ser	Ile	Thr	Asn	Ala	Ser	Gly
		195					200					205			
Asp	Ala	Ile	Val	Gly	Asn	Pro	Asp	Ser	Gln	Gly	Leu	Gly	Lys	Leu	Arg
210					215						220				
Gln	Gly	Phe	Leu	Glu	Leu	Ser	Asn	Val	Arg	Leu	Val	Glu	Glu	Met	Thr
225					230				235					240	
Asp	Leu	Ile	Thr	Ala	Gln	Arg	Ala	Tyr	Glu	Ala	Asn	Ser	Lys	Ser	Ile
			245						250					255	
Gln	Thr	Ala	Asp	Ala	Met	Leu	Gln	Thr	Val	Asn	Ser	Leu	Lys	Arg	
			260				265							270	

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids

562

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673

```

Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser Tyr Cys Leu
1          5          10          15
Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu
          20          25          30
Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu
          35          40          45
Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile
50          55          60
Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674

```

Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
1          5          10          15
Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
          20          25          30
Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
          35          40          45
Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
50          55          60
Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
65          70          75          80
Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
          85          90          95
Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
          100          105          110
Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
          115          120          125
Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu

```

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130		135		140
Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp				
145		150		155
Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln				
		165		170
Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu				
		180		185
Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg				
		195		200
Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser				
210		215		220
Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn				
225		230		235
Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp				
		245		250
Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn				
		260		265
Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser				
		275		280
Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val				
290		295		300
Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro				
305		310		315
Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys				
		325		330
Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro				
		340		345
Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser				
		355		360
Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp				
370		375		380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val				
385		390		395
				400

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

Met	Gln	Asn	Gly	Tyr	Tyr	Ala	Ala	Thr	Gly	Ala	Met	Ala	Thr	Gln	Phe
1				5					10					15	
Asn	Arg	Leu	Asp	Leu	Thr	Ser	Asn	Asn	Leu	Ala	Asn	Leu	Asn	Thr	Asn
		20						25					30		
Gly	Phe	Lys	Arg	Asp	Asp	Ala	Ile	Thr	Gly	Asp	Phe	Leu	Arg	Leu	Tyr
		35				40						45			
Gln	Glu	Tyr	Arg	Glu	Gln	Leu	Pro	Leu	Glu	Asp	Gln	Thr	Lys	Ala	Ser
	50				55				60						
Ala	Lys	Tyr	Leu	Asn	Arg	Unk	Leu	Asn	Arg	Val	Pro	Ile	Leu	Ser	Unk
65				70					75					80	

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Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val
85 90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

Met	Gln	Asn	Gly	Tyr	Tyr	Ala	Ala	Thr	Gly	Ala	Met	Ala	Thr	Gln	Phe	1	5	10	15
Asn	Arg	Leu	Asp	Leu	Thr	Ser	Asn	Asn	Leu	Ala	Asn	Leu	Asn	Thr	Asn	20	25	30	
Gly	Phe	Lys	Arg	Asp	Asp	Ala	Ile	Thr	Gly	Asp	Phe	Leu	Arg	Leu	Tyr	35	40	45	
Gln	Glu	Tyr	Arg	Glu	Gln	Leu	Pro	Leu	Glu	Asp	Gln	Thr	Lys	Ala	Ser	50	55	60	
Ala	Lys	Tyr	Leu	Asn	Arg	Unk	Leu	Asn	Arg	Val	Pro	Ile	Leu	Ser	Unk	65	70	75	80
Ile	Tyr	Thr	Unk	Arg	Unk	Leu	Gly	Unk	Val							85	90		

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676

Met	Leu	Pro	Thr	Lys	Thr	Arg	Ile	Arg	Asp	Pro	Asn	Lys	Gln	Glu	Leu	1	5	10	15
Thr	Gln	Pro	Lys	Ile	Lys	Gly	Leu	Ser	Met	Gly	Lys	Ile	Leu	Ala	Ser	20	25	30	
Leu	Leu	Gly	Gly	Gly	Thr	Asn	Leu	Phe	Thr	Gly	Leu	Ser	Ser	Asp	Leu	35	40	45	
Phe	Ser	Met	Ile	Leu	Asn	Phe	Leu	Phe	Phe	Leu	Met	Leu	Met	Met	Gly				

565

50				55				60							
Leu	Asn	Glu	Ala	Leu	Gly	Lys	Lys	Phe	Asn	Leu	Pro	Met	Asp	Asn	Ile
65					70				75						80
Lys	Asn	Phe	Met	Ala	Glu	Val	Leu	Lys	Asn	Gly	Phe	Asp	Ser	Ile	Lys
				85					90					95	
Asn	Met	Gly	Ser	Ala	Leu	Val	Gly	Asn	Gly	Phe	Gly	Ser	Ser	Lys	Ser
			100						105					110	
Asp	Lys	Thr	Thr	Asn	Lys	Met	Ser	Val	Pro	Gln	Val	Arg	Leu		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

[illegible]

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

```

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Unk Phe Gly Ala Gly Gly
1      5      10      15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
      20      25      30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
      35      40      45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
      50      55      60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65      70      75      80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Unk Thr Tyr
      85      90      95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Unk Asp Lys Thr
      100     105     110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
      115     120     125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
130     135     140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145     150     155     160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
      165     170     175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Unk
180     185     190
Gln Pro Gly
      195

```

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678

```

Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
1      5      10      15
Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu

```

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```

      20      25      30
Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
      35      40      45
Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
      50      55      60
Glu Val Ile Tyr Glu Val Ile Glu
65      70

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679

```

Met Ala Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe
1      5      10      15
Val Ser Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys
      20      25      30
His Thr Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val
      35      40      45
Ala Ile Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp
      50      55      60
Val Leu Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile
65      70      75      80
Phe Trp Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu
      85      90      95
Thr Ala Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680

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```

Met Ile Thr Ile Val Ile Ala Lys Ala Gly Asn Ile Val Lys Unk Asp
1           5           10           15
Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly Gly
          20           25           30
Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala Lys
          35           40           45
Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys Asp
          50           55           60
Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Leu Leu Lys Thr
65           70           75           80
Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg Asp
          85           90           95
Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile Leu
          100          105          110
Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Unk Leu Ala Unk
          115          120          125
Unk Leu Glu Thr Thr Asp Leu Tyr Tyr Ala Ser Asp Val Phe
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681

```

Val Asn Phe Asn Ala Lys Asn Ile Ser Ile Asp Asn Leu Val Glu Ile
1           5           10           15
Asn Asn Arg Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val
          20           25           30
Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr Unk Ser Lys Asn Ala Glu
          35           40           45
Ile Ser Leu Tyr Asp Gly Ala Thr Unk Ile Trp Leu Gln Thr Gly
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:

569

(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682

```

Met Arg Thr Leu Ile Leu Ser Leu Leu Lys His Ala Ile Leu Met Gly
1      5      10
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
20      25      30
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
35      40      45
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
50      55      60
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
65      70      75      80
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
85      90      95
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
100     105     110
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
115     120     125
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
130     135     140
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
145     150     155     160
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr
165     170     175
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
180     185     190
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
195     200     205
Thr Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
210     215     220
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
225     230     235     240
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
245     250     255
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
260     265     270
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
275     280     285
Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
290     295     300
Ile Ser Pro Tyr Asp Leu
305     310

```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...169

570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683

```

Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys
1           5           10           15
Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala
          20           25           30
Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly
          35           40           45
Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln
          50           55           60
Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro
          65           70           75           80
Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met
          85           90           95
His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu
          100          105          110
Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe
          115          120          125
Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly
          130          135          140
Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn
          145          150          155          160
Ala Cys Thr Phe Pro Lys Val Glu Phe
          165

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

```

Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
1           5           10           15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
          20           25           30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
          35           40           45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
          50           55           60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
          65           70           75           80
Tyr Pro Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

```

Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
1          5          10          15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
20          25          30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
35          40          45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
50          55          60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
65          70          75          80
Tyr Pro Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

```

Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1          5          10          15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
20          25          30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
35          40          45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
50          55          60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

572

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

```

Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1          5          10          15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
20          25          30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
35          40          45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
50          55          60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

```

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1          5          10          15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
20          25          30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
35          40          45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
50          55          60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65          70          75          80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
85          90          95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
100          105          110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
115          120          125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly

```

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130	135	140
Asn Pro Asn Asn Ala Thr	Asn Asn Thr Leu Glu Asp Lys Val Val Gly	
145	150	155
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile		160
	165	170
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp		175
	180	185
Arg Leu Unk Unk		190
195		

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile	
1	5 10 15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly	
	20 25 30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys	
	35 40 45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn	
	50 55 60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu	
65	70 75 80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro	
	85 90 95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn	
	100 105 110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu	
	115 120 125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly	
	130 135 140
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly	
145	150 155 160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile	
	165 170 175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp	
	180 185 190
Arg Leu Unk Unk	
195	

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

574

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687

```

Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser Leu
1      5      10      15
Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala Asn
      20      25      30
Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly Leu
      35      40      45
Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe Glu
      50      55      60
Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val Phe
      65      70      75      80
Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys Ile
      85      90      95
Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser Thr
      100     105     110
Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr Phe
      115     120     125
Ile Ala Phe Leu Phe Ala Ile Phe Tyr Ala Gly Gly Tyr Gln
      130     135     140

```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688

```

Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile Phe
1      5      10      15
Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly Tyr
      20      25      30
Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu Ser
      35      40      45
Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys Lys
      50      55      60
Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys Lys
      65      70      75      80
Ala Cys Glu Glu Val Phe

```

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85

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689

```

Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser
1           5           10           15
Gly Pro Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val
          20          25          30
Ala Lys Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn
          35          40          45
Arg Ala Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu
          50          55          60
Phe Gly Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His
65          70          75          80
His Leu Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys
          85          90          95
Asp Tyr Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Lys Phe Thr
          100         105         110
Asp Arg Leu Asn Glu Gly Glu Ala Leu
          115         120

```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690

```

Met Thr Ile Thr Thr Leu Ser Phe Leu Phe Thr Thr Pro Glu Val Phe
1           5           10           15
Val Asn Gln Asp Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val
          20          25          30

```

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Lys Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp
 35 40 45
 Arg Asn Ala Ile Trp Arg Val Lys Gly Phe Ala
 50 55

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691

Val Phe Ser Gly Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser
 1 5 10 15
 Ala Phe Val Ile Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro
 20 25 30
 Leu Gly Arg Glu Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val
 35 40 45
 Ile Gly Tyr Gly Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala
 50 55 60
 Pro Asn Ala Lys Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile
 65 70 75 80
 Asn Val Leu Ala Ile Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu
 85 90 95
 Tyr Tyr Leu Lys Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala
 100 105 110
 Leu Gln Lys Cys Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala
 115 120 125
 Ala Asn Unk Unk Val Ala His Thr Glu Asp Unk Leu Ser His
 130 135 140

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692

577

```

Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn
1           5           10           15
Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr
20           25           30
Ile Asp Unk Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly
35           40           45
Val Tyr Gly Val Lys Unk Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser
50           55           60
Gly Gly Arg Ile Phe Trp Val Trp Unk Unk Unk Phe Leu Ser Cys Ile
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

```

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1           5           10           15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
20           25           30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
35           40           45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
50           55           60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65           70           75           80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
85           90           95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
100          105          110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
115          120          125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
130          135          140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145          150          155          160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
165          170          175
Leu Val Lys

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

```

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1          5          10          15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
          20          25          30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
          35          40          45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
          50          55          60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65          70          75          80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
          85          90          95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
          100          105          110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
          115          120          125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
          130          135          140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145          150          155          160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
          165          170          175
Leu Val Lys

```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694

```

Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile Met Ser
1          5          10          15
Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg Ile Asp
          20          25          30
Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu Gly Glu

```

579

```

      35              40              45
Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile Gly Thr
      50              55              60
Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg
      65              70              75

```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695

```

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1              5              10              15
Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
      20              25              30
Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
      35              40              45
Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
      50              55              60
Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
      65              70              75              80
Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
      85              90              95
Gly Asn Asp

```

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696

```

Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr
1              5              10              15

```

580

```

Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg
      20      25      30
Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr
      35      40      45
Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu
      50      55      60
His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu
      65      70      75      80
Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly
      85      90      95
Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp
      100      105      110
Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys
      115      120      125
Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser
      130      135      140
Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser
      145      150      155      160
Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala
      165      170      175
Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro
      180      185      190
Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly
      195      200      205
Asn

```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697

```

Val Gly Ser Leu Lys Phe Leu Asn Ala Met Gly Val Asp Leu Lys Val
1      5      10      15
Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Lys Thr Leu
      20      25      30
Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala Lys Glu
      35      40      45
Val Ile Gln Ala Leu Gln Asn Gln Gly Leu Glu Leu Glu Ile Leu Ser
      50      55      60
Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala
      65      70      75

```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698

```

Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu Gln Ile Leu
1          5          10          15
Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro Met Ile Pro
20        25        30
His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg Glu Asn Phe
35        40        45
Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp Phe Met Thr
50        55        60
Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu Lys Val Asn
65        70        75        80
Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys Lys Glu Leu
85        90        95
Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile Tyr Val Pro
100       105       110
Asn Lys Leu Val Asn Phe Val Thr Ala
115       120

```

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699

```

Met Lys Glu Ser Ile Lys Tyr Leu Leu Glu Ser Val Gly Leu Val Leu
1          5          10          15
Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln Lys Phe Leu Asp Leu
20        25        30
Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu Ile Lys Arg Tyr Asn
35        40        45
Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val Asn Asp Lys Asn Ile
50        55        60
Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val Val Ser Gly Ser Tyr
65        70        75        80
Ile Phe Glu Ser Lys Asp Unk Lys Leu Ala Ile Glu Gly Leu Gln Asn
85        90        95

```

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Val Arg Gln Pro Leu Ala
100

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700

Val	His	Asp	Gly	Val	Leu	Gly	Trp	Val	Gly	Phe	Thr	Leu	Ile	Ala	Ser	1	5	10	15
Met	Tyr	His	Met	Thr	Pro	Arg	Leu	Phe	Lys	Arg	Glu	Ile	Tyr	Ser	Gly	20	25	30	
Arg	Leu	Val	Asp	Phe	Gln	Phe	Trp	Ile	Met	Thr	Leu	Gly	Ile	Val	Leu	35	40	45	
Tyr	Phe	Ser	Ser	Met	Trp	Ile	Ala	Gly	Ile	Thr	Gln	Gly	Met	Met	Trp	50	55	60	
Arg	Asp	Val	Asp	Gln	Tyr	Gly	Asn	Leu	Thr	Tyr	Gln	Phe	Ile	Asp	Thr	65	70	75	80
Val	Lys	Ala	Leu	Ile	Pro	Tyr	Tyr	Asn	Ile	Arg	Gly	Val	Gly	Gly	Leu	85	90	95	
Met	Tyr	Phe	Ile	Gly	Phe	Ile	Ile	Phe	Ala	Tyr	Asn	Ile	Phe	Met	Thr	100	105	110	
Ile	Thr	Ala	Gly	Lys	Lys	Leu	Glu	Arg	Glu	Pro	Asn	Tyr	Ala	Thr	Pro	115	120	125	
Met	Ala	Lys														130			

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701

Met Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser

583

```

1           5           10           15
Ser Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln
20           25           30
Phe Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg
35           40           45
Ala Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile
50           55           60
Glu Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His
65           70           75           80
Arg Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe
85           90           95
Ile Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His
100          105          110
Ser Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu
115          120          125
Leu Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu
130          135          140
Arg Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser
145          150          155          160
Val Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn
165          170          175
Glu Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg
180          185          190
Val Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr
195          200          205
Lys Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys
210          215          220
Arg Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe
225          230          235          240
Ala Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu
245          250          255
Lys Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu
260          265          270
Ile Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr
275          280          285
Ile Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met
290          295          300
Ile Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp
305          310          315          320
Phe Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys
325          330          335
Glu Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro
340          345          350
Ser Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala
355          360          365
Leu Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg
370          375          380
Ile Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu
385          390          395          400
Glu Ala Asp Asn Glu Glu Leu Pro Pro Pro Glu Asn Leu Arg Glu Val
405          410          415
Lys Gly Met Lys Gly Thr Glu Lys Ala Asn Cys Gly Val Lys Glu Lys
420          425          430
Gln Lys Glu Arg Thr Cys Ser Asn Asp
435          440

```

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702

```

Val Leu Leu Leu Ser Arg Met Gly Ile Ala Phe Ala His Ser Ile Phe
1           5           10           15
Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg Asn Lys
          20           25           30
Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu Ala Met
          35           40           45
Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp
50           55           60
Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile Met Leu
65           70           75           80
Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala Gly Thr
          85           90           95
Leu Ala Ser Val Pro Ile Leu Met Lys Arg Pro Leu Leu Val Gly Ile
          100          105          110
Tyr Leu His Val Asn His Gly Tyr Phe Trp Ala Phe His His Leu
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1           5           10           15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
          20           25           30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
          35           40           45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
50           55           60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65           70           75           80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
          85           90           95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
          100          105          110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp

```

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```

      115      120      125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
130      135      140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145      150      155      160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
      165      170      175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180      185      190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
195      200      205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
210      215      220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225      230      235      240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
      245      250      255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
260      265      270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1      5      10      15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
20      25      30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
35      40      45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
50      55      60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65      70      75      80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
85      90      95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
100      105      110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
115      120      125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
130      135      140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145      150      155      160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
165      170      175

```

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```

Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180      185      190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
      195      200      205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
      210      215      220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
      225      230      235      240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
      245      250      255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
      260      265      270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

```

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1      5      10      15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
      20      25      30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
      35      40      45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
      50      55      60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
      65      70      75      80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
      85      90      95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

587

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

```

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1           5           10           15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
          20           25           30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
          35           40           45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
          50           55           60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
65           70           75           80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
          85           90           95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705

```

Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu
1           5           10           15
Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn
          20           25           30
Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu
          35           40           45
Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg
          50           55           60
Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile
65           70           75           80
Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys
          85           90           95
Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys
          100          105          110
Lys Tyr Ser
          115

```

(2) INFORMATION FOR SEQ ID NO:706:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706

```

Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1          5          10          15
Lys His Ser Val Cys Leu Lys Pro Phe Arg Phe Cys Phe Leu Lys
20          25          30
Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
35          40          45
Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
50          55          60
Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65          70          75          80
Arg Val Ser Asn Ala Tyr
85

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707

```

Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1          5          10          15
Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
20          25          30
Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
35          40

```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

589

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708

```

Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser His
1      5      10      15
Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly Thr Ala Thr Ile Met
      20      25      30
Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala Ser Ser Lys Glu Val
      35      40      45
Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala Ile Tyr Tyr Gly Tyr
      50      55      60
Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp Asn Tyr Leu Lys Leu
      65      70      75      80
Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met Val Met Thr Asp Asn
      85      90      95
Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val Lys Asp Gly Gly Leu
      100      105      110
Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr Ile Tyr Thr Ser Ile
      115      120      125
Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn Asp Pro Ile Asn Asn
      130      135      140
Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala Gln Ile Gln Gly Val
      145      150      155      160
Gln Ser Val Asp Ser Ile Unk Gln Ala Gly Gly Asn Gln Ala Ile Asn
      165      170      175
Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser Pro Leu Phe Ala Pro
      180      185      190
Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu Thr Thr Ile Ala Gly
      195      200      205
Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn Pro Asn Phe Lys Asn
      210      215      220
Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr Thr Gln Gln Met Ser
      225      230      235      240
Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe Ala Arg Ser Asp Phe
      245      250      255
Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg Phe Ala Asp Ala Ile
      260      265      270
Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asn Arg Val
      275      280      285
Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly Ala Ser Phe Ile Ser
      290      295      300
Gly Gly Thr Unk Thr Leu Tyr Gly Ile Asn Unk Gly Tyr Asp Arg Phe
      305      310      315      320
Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr Ser Gly
      325      330      335
Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser Asn Val Asn Val Gly
      340      345      350
Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu Leu Thr Met Ser Leu
      355      360      365
Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile Asn Ser Tyr Asp Pro
      370      375      380
Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr Asp Thr Trp Thr Thr
      385      390      395      400
Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met Phe Lys Asp Lys Ser
      405      410      415

```

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```

Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr Tyr Tyr Ile Gly Leu
      420      425      430
Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile Tyr Asn Gln Phe Arg
      435      440      445
Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu Thr Ile Asn Phe Ala
      450      455      460
Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser Tyr Tyr Phe Val Ile
465      470      475      480
Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser Met Gly Asp Lys Met
      485      490      495
Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr Arg Asp Gly Gly Arg
      500      505      510
Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly Glu Ile Arg Leu Phe
      515      520      525
Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala Arg Phe Gly Leu Asp
      530      535      540
Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly Met Unk Unk Unk Phe
545      550      555      560

```

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

```

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1      5      10      15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
      20      25      30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
      35      40      45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
      50      55      60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
      65      70      75      80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
      85      90      95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
      100      105      110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
      115      120

```

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

```

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1          5          10          15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
20          25          30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
35          40          45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
50          55          60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
65          70          75          80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
85          90          95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
100          105          110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
115          120

```

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

```

Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1          5          10          15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
20          25          30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
35          40          45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
50          55          60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
65          70          75          80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
85          90          95

```

592

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

```

Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1          5          10          15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
20          25          30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
35          40          45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
50          55          60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
65          70          75          80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
85          90          95

```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

```

Leu Pro Ile Ile Leu Unk Val Ile Val Met Met Phe Phe Ser Lys Ile
1          5          10          15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
20          25          30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
35          40          45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
50          55          60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65          70          75          80

```


593

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

```

Leu Pro Ile Ile Leu Unk Val Ile Val Met Met Phe Phe Ser Lys Ile
1          5          10          15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
20          25          30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
35          40          45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
50          55          60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65          70          75          80

```

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712

```

Met Glu Ser Asn Gln Ser Leu Pro Met Ala Leu Ile Ser Cys Ser Pro
1          5          10          15
Asn Ala Lys Gly Ala Asp Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu
20          25          30
Leu Ile Glu Arg Asn Phe Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser
35          40          45
Thr Leu Thr Asn Gly Leu Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn
50          55          60
Arg Gly Asn Lys Glu Glu Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu
65          70          75          80
Leu Gln Leu Met Arg Gln Ser Gly Met Gly Ile Asn Gln Val Val Asn
85          90          95

```

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```

Gln Ile Leu Arg Asp Lys Ser Lys Ile Ala Pro Ile Val Val Ile Arg
      100      105      110
Glu Gly Ser Arg Val Phe Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro
      115      120      125
Ile Pro Arg Glu Asn Glu Val Ile Ala Glu Phe Leu Lys
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713

```

Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro
1      5      10      15
Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu
      20      25      30
Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly
      35      40      45
Asn Glu Arg
50

```

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714

```

Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
1      5      10      15
Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
      20      25      30
Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
      35      40      45
Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp

```

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```

      50              55              60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65              70              75              80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
      85              90              95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
      100             105             110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala
      115             120             125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg
      130             135             140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu
145             150             155             160
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln
      165             170             175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr
      180             185             190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
      195             200             205
Ile Lys Ser Gly Thr Leu Leu Ala Ala Gly Thr Leu Met Lys Phe Met
      210             215             220
Lys Thr Leu Trp Cys Val Ser Ile Ile
225             230

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1              5              10              15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
      20              25              30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
      35              40              45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
      50              55              60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
65              70              75              80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
      85              90              95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
      100             105             110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
      115             120             125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
      130             135             140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
145             150             155             160

```

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```

Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
      165      170      175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
      180      185      190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
      195      200      205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
      210      215      220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
      225      230      235      240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
      245      250      255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
      260      265

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1      5      10      15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
      20      25      30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
      35      40      45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
      50      55      60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
      65      70      75      80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
      85      90      95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
      100      105      110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
      115      120      125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
      130      135      140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
      145      150      155      160
Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
      165      170      175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
      180      185      190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
      195      200      205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
      210      215      220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile

```

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```

225          230          235          240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
          245          250          255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
          260          265

```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716

```

Met Lys Glu Ile Val Thr Ile Glu Asn Val Ser Phe Asn Tyr His Asn
1          5          10          15
Arg Ala Ile Phe Lys Asp Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe
          20          25          30
Leu Cys Val Leu Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly
          35          40          45
Leu Ile Leu Gly Leu Leu Lys Pro Ser Leu Gly Ser Val Lys Ile Phe
          50          55          60
Asn Glu Thr Leu Ser Asn Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr
65          70          75          80
Ile Ala Gln Gly Asn Ser Leu Phe Pro His Leu Asn Ala Leu Gln Asn
          85          90          95
Met Thr Phe Cys Leu Asn Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln
          100          105          110
Lys Glu Ala Lys Ala Leu Ala Leu Lys Met Gly Leu Asp Glu Ser Leu
          115          120          125
Met Asp Lys Phe Pro Asn Glu Leu Ser Gly Gly Gln Ala Lys Glu Trp
          130          135          140
Ala Leu Leu Gly Gly Leu Ser Thr Gly Gln Asn Ser Phe Tyr
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717

```

Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly Leu Ser Glu
1      5      10      15
Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile Leu Ser Leu
20     25     30
Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser His Tyr Leu
35     40     45
Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro Asn Ala Pro
50     55     60
Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe Lys Lys Thr
65     70     75     80
Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val Val Ala Leu
85     90     95
Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys Ile Phe Asp
100    105    110
Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu Ile Phe Leu
115    120    125
Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala Leu Pro Leu
130    135    140
Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu Asp Lys Asp
145    150    155    160
Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr Ala Phe Phe
165    170    175
Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys Leu Lys
180    185    190

```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718

```

Met Val Leu Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val
1      5      10      15
Leu Ser Glu Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp
20     25     30
Val Ala Asp Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu
35     40     45
Lys Lys Lys Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn
50     55     60
Lys Ile Ala Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr
65     70     75     80
Ile Leu Ser Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro
85     90     95
Lys Asp Leu Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys
100    105    110
Asp Ile Val Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr

```

115 120 125
Ala Leu Ile Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp
130 135 140
Phe Thr Phe Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val
145 150 155
Thr Phe Asn Leu Val Ile Asp Ile Asp Arg Pro Met Ser Gln Gln Phe
165 170 175
Leu Asn Unk Ile Gly Lys Leu Gln Ser Phe Gln Ser Arg Gln Ala
180 185 190
Leu Gln Trp Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Gln Thr Pro
195 200 205
Lys Gln Ala Leu Lys Asn Ala Gln Leu Ser Gln Ile Gln Ile Leu
210 215 220
Thr Gly Cys Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys
225 230 235 240
Lys Gly Arg

(2) INFORMATION FOR SEQ ID NO:719:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...236

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:719

Val Ser Gln Val Ala Ser Val Gly Gly Phe Val Lys Asp Tyr Gln Val
1 5 10
Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr Asn Leu Ser Leu Gln
20 25 30
Val Ala Asn Ala Ile Lys Asn Ser Asn Asp Thr Gly Gly Val
35 40 45
Ile Leu Gln Asn Gly Phe Gln Lys Ile Ile Arg Ser His Gly Tyr Ile
50 55 60
Gln Ser Leu Asn Asp Leu Gln Ile Val Val Lys Lys Gln Gly Ala
65 70 75 80
Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser Val Arg Leu Ala Pro Lys
85 90 95
Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly Asp Lys Gln Val Gly
100 105 110
Gly Ile Val Met Val Arg Tyr His Ala Asp Thr Tyr Lys Val Leu Lys
115 120 125
Ala Ile Lys Gln Lys Ile Ala Thr Leu Gln Ala Ser Asn Pro Asp Val
130 135 140
Lys Ile Thr Ser Val Tyr Asp Arg Ser Gln Leu Ile Gln Lys Gly Ile
145 150 155 160
Asp Asn Leu Ile His Thr Leu Ile Gln Ser Val Ile Val Leu Val
165 170 175
Ile Ile Ala Ile Phe Leu Leu His Phe Arg Ser Ala Leu Val Ile
180 185 190
Ile Thr Leu Pro Leu Arg Val Cys Ile Ser Phe Leu Leu Met Ser Tyr
195 200 205 210 215 220 225 230 235 240

600

phe Asn Ile Glu Ala Ser Ile Met Ser Leu Gly Gly Ile Ala Ile Ala
 210 215 220
 Ile Gly Ala Met Val Asn Ala Ala Ile Val Met Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:720:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...175

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:720

Val Glu Thr Phe Leu Arg Ile Phe Glu Lys Asp Ile Phe Asn Thr Pro
 1 5 10 15
 Tyr Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys
 20 25 30
 Gly Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys
 35 40 45
 Ser Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Glu Ser Glu
 50 55 60
 Glu Ala Lys Asn Leu Lys Ile Ala Lys Lys Lys Cys Glu Glu Ile Ile
 65 70 75 80
 Lys Tyr Ala Asn Glu Lys Lys Thr Glu Val Glu Ala Phe Leu Lys
 85 90 95
 Val Ala Glu Phe Leu Glu Lys Val Glu Lys Leu His Glu Lys Asn Lys
 100 105 110
 Leu Glu Glu Leu Asp Phe Glu Glu Leu Asn Leu Ser Ala Glu Ile
 115 120 125
 Asp Asn Val Lys Glu Leu Phe Asp Asp Lys Arg Phe Asn Ser Tyr Phe
 130 135 140 145
 Met Asp Ala Ile Glu Ser Tyr Ile Phe His Glu Leu His Ile Ala
 150 155 160
 Glu Ile Val Cys Lys Lys Thr Ser Asn Glu Asp Gly Ile Lys Gly
 165 170 175

(2) INFORMATION FOR SEQ ID NO:721:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature
(B) LOCATION 1...226

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:721

Met Lys Thr Pro Cys Asn Ala Tyr Phe Leu Lys Thr Pro Lys Asn
1
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
5
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
10
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
15
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
20
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
25
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
30
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
35
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
40
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
45
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
50
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
55
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
60
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
65
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
70
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
75
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
80
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
85
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
90
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
95
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
100
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
105
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
110
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
115
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
120
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
125
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
130
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
135
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
140
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
145
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
150
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
155
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
160
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
165
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
170
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
175
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
180
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
185
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
190
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
195
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
200
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
205
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
210
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
215
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
220
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
225

(2) INFORMATION FOR SEQ ID NO:722:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature
(B) LOCATION 1...79

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:722

Val Met Val Tyr Lys Leu Pro Lys His Gln Asn Lys Val Met Ile
1
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
5
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
10
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
15
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
20
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
25
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
30
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
35
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
40
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
45
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
50
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
55
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Leu
60

602

Leu Ala Phe Lys Ala Leu Val Glu Leu Lys Arg Ala Asp Leu Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:723:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(1x1) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Glu Leu Ile Leu Pro Tyr
1 5 10 15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
20 25 30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Glu Lys
35 40 45
Ala Unk Ser His Ala His Trp Trp Glu Cys Gly Ala Asn Phe Arg Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:723:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(1x1) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Glu Leu Ile Leu Pro Tyr
1 5 10 15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
20 25 30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Glu Lys
35 40 45
Ala Unk Ser His Ala His Trp Trp Glu Cys Gly Ala Asn Phe Arg Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:724:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

((1)) MOLECULE TYPE: protein

((11)) HYPOTHETICAL: YES

((1)) ORIGINAL SOURCE:

((A)) ORGANISM: Helicobacter pylori

((X)) FEATURE:

((A)) NAME/KEY: misc_feature

((B)) LOCATION 1...138

((X1)) SEQUENCE DESCRIPTION: SEQ ID NO:724

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
 1 5 10 15 20 25 30 35 40 45
 Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
 Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135
 Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
 Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
 Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala
 Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
 Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
 Val Val Gly Phe Leu Gly Met Glu His

(2) INFORMATION FOR SEQ ID NO:724:

((1)) SEQUENCE CHARACTERISTICS:

((A)) LENGTH: 138 amino acids

((B)) TYPE: amino acid

((D)) TOPOLOGY: linear

((1)) MOLECULE TYPE: protein

((11)) HYPOTHETICAL: YES

((1)) ORIGINAL SOURCE:

((A)) ORGANISM: Helicobacter pylori

((X)) FEATURE:

((A)) NAME/KEY: misc_feature

((B)) LOCATION 1...138

((X1)) SEQUENCE DESCRIPTION: SEQ ID NO:724

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
 1 5 10 15 20 25 30 35 40 45
 Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
 Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro

604

Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
 50 55 60
 Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Gln Thr Ile Ser Ser His
 65 70 75
 Ala Asp Val Ser Ala Gln Gln His Val Asn Ile Ile Gln Ala Unk Ala
 80 85 90 95
 Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
 100 105 110
 Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
 115 120 125
 Val Val Gly Gly Phe Leu Gly Met Gln His 130 135

(2) INFORMATION FOR SEQ ID NO:725:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...210

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:725

Met Phe Val Val Phe Ile Gln Gly Phe Gly Leu Ala Ile Ser Leu Cys
 1 5 10 15
 Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val Gln Arg Gly Met Ala
 20 25 30
 Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys Phe Met Cys Asp Ile
 35 40 45
 Val Leu Met Ser Met Gly Val Phe Gly Val Gly Ala Tyr Phe Ala Lys
 50 55 60
 Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe Gly Ala Val Phe Thr
 65 70 75
 Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu Phe Gln Thr Phe Lys
 80 85 90 95
 Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser Leu Lys Lys Thr Leu
 100 105 110
 Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro Gln Val Tyr Leu Gln
 115 120 125
 Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser Phe Asn Leu Val Gln
 130 135 140
 Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala Phe Ser Trp Leu
 145 150 155
 Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly Ser Lys Leu Leu Asn
 160 165 170 175
 Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe Val Thr Ala Ile Met
 180 185 190
 Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe Leu Ala Leu Leu Ser
 195 200 205
 Lys Thr 210

(2) INFORMATION FOR SEQ ID NO:726:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726

Val Lys Pro Lys Ser Met Lys Gln Lys Leu Arg Gly Ala Met Val Asn
 1 5 10 15
 Ile Leu Arg Ile Lys Met Ile Gln Ile Ser Gln Trp Leu Gln Lys Leu
 20 25 30 35
 Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Gln Pro Gln Ser Phe
 40 45
 Leu Lys Pro Ile Ile Ser Pro Ile Gln Asp Tyr Gln Lys Ser Val Arg
 50 55
 Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Gln Gln Gly
 60 65
 Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
 70 75 80
 Asn Gly Ala Asn Met Gln Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro
 85 90 95
 Pro Lys Ser Leu Tyr Ile Gln His Gln Lys Asp Gly Gln Phe Leu Arg
 100 105 110
 Gln Met Leu Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Gln
 115 120 125
 Val Ile Leu Ile Asp Ala Leu Ser Leu Gly Ile Phe Asn Leu Ala
 130 135 140
 Val Ile Leu Ile Asp Ala Leu Ser Lys Asp Ala Leu Tyr Tyr Leu
 145 150 155
 Arg Arg Leu Leu Asp Lys Asn Asn Asp Phe Ile Tyr Gln Gln Arg Ile
 160 165 170 175
 Leu Thr Gln Ser Lys Gln Ile Gln Ala Leu Lys His Leu His Gln
 180 185 190
 Tyr Leu Lys Val Asn Leu Gln Gln Lys Leu Ala Gly Phe Arg Asp Phe
 195 200 205
 Val His Tyr Asn Gln Asn Ala Lys Asp Ser Leu Pro Leu Lys Ala Leu
 210 215 220
 Phe Leu Ser Gly Val Asp Ala Leu Ser Lys Asp Ala Leu Tyr Tyr Leu
 225 230 235 240
 Gln Lys Ile Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val
 245 250 255
 Asn Leu Gln Ser Gln Lys Asn Asn Gln Ser Ala Gln Asp Leu Lys Arg
 260 265 270 275
 Tyr Ala Gln Phe Phe Lys Asp Arg Thr Ser Phe Gln Unk Leu Lys Tyr
 280 285 290 295
 Leu Asn Val Gln Ile Ile Ser Asp

(2) INFORMATION FOR SEQ ID NO:727:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
(2) INFORMATION FOR SEQ ID NO: 729:

Met Gln Ala Gln Leu Arg Phe Thr Gly Val Gly Gln Gly Val Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Lys Val Asp Ile Leu Leu Asp Lys Asp Gln Ile Ile Phe Pro Tyr Ala
Lys Gln Gly Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr
Asn Gln Phe

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 728

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...83

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 728:

Val Leu Ile Ser Val Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
His Tyr Thr Tyr Lys Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Gln
Ile Phe Gly Ala Gly Val Phe Val Gly Gln Val Ser Ser Val Gln Asp
Ala Gln Ile Asn Ile Gly Asn Gln Val Ile Thr Ser Gly Leu Asp Gly
Gly Thr Asn Phe Lys Gln Gln Leu Val Val Asp Phe Ile Val Pro Ser
Ala Lys Leu Leu Arg His Val Phe Leu Ser Gly Val Lys Asn

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 727

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:730

(A) NAME/KEY: misc_feature
(B) LOCATION 1...220

(ix) FEATURE:

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:730:

Met Gln Ala Trp Val Asp Lys Pro Val Leu Leu Gln Pro Asp Ser Asn
1 5 10 15
Ala Gln Tyr Ala Ala Val Ile Gln Ile Asp Val Ala Gln Ile Thr Gln
20 25 30
Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp Asp Val Ala Thr Leu Ser
35 40 45
Gln Val Leu Ala Asp Thr Thr Gln Lys Arg Pro His Ala Ile Asp Gln
50 55 60
Val Phe Ile Gln Ser Cys Met Thr Asn Ile Gln His Phe Arg Ala Phe
65 70 75
Gln Gln Ile Val Lys Asn Ala Pro Pro Ser Gln Ala Arg Leu Trp Val
80 85 90
Val Pro Pro Ser Lys Met Asp Gln Gln Gln Leu Ile Asn Gln Gln Tyr
100 105 110
Tyr Ala Ile Phe Gln Ala Ala Gln Arg Thr Gln Val Pro Gln Cys
115 120 125
Ser Leu Cys Met Gln Asp Arg Val Arg Asp Asn Ala Val Val
130 135 140
Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn Arg Met Gln Arg Gln Ala
145 150 155 160
Lys Val Tyr Leu Gln Ser Ala Gln Leu Gln Ala Cys Ala Leu Leu
165 170 175
Gln Arg Ile Pro Thr Lys Gln Gln Tyr Met Asn Leu Val Ser Gln Lys
180 185 190
Leu Gln Ser Gln Lys Asp Lys Ile Tyr Arg Ser 200

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:729

(A) NAME/KEY: misc_feature
(B) LOCATION 1...203

(ix) FEATURE:

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:731

[illegible]

(2) INFORMATION FOR SEQ ID NO: 731:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 731

Val Met Asn Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1 5 10 15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Gly Ala
20 25 30
Glu Asp Ile Val Gln Val Ser His Leu Thr Ser Phe Tyr Gly Pro
35 40 45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ile Asn
50 55
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65 70 75
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
85 90 95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
100 105 110
Ala Ile Ile Unk
115

(2) INFORMATION FOR SEQ ID NO: 732:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 732

Met Gln Lys Ser Ile Phe Lys Ile Thr Leu Leu Val Phe Leu Phe
1 5 10 15
Leu Arg Asn Ala Val Gly Leu Asp Asp Lys Lys Ala Ala Pro Lys Ser
20 25 30

610

Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
 35 40 45
 Gln Ala Tyr Gln Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
 50 55 60
 Thr Gln Tyr Gln Phe Pro Lys Ile Lys Gln Ile Leu Gln Ser Gln
 65 70 75 80
 Gln Gln Trp Leu Gly Val Ala His Gln Cys Val Ala Leu Val Met
 85 90 95
 Leu Ile Ser Pro Lys Ala Ser Ile Gln Asn Ser Pro Ile Tyr Lys Asn
 100 105 110
 Cys Tyr Gln Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
 115 120 125
 Tyr Ile Gln Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Gln
 130 135 140
 His Gln Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Gln Pro Pro
 145 150 155 160
 Lys Ser Gln Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
 165 170 175
 Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
 180 185 190
 Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
 195 200 205
 Gln Gln Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
 210 215 220
 Lys Gln Gln Ala Leu Lys Gln Leu Gln Asn Ala Ala Lys Ser Phe Lys
 225 230 235 240
 Asn Lys Pro Ala Leu Val Gln Lys 245

(2) INFORMATION FOR SEQ ID NO:733:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:733

Met Gln Gln Ile Leu Ile Pro Leu Lys Gln Lys Ser Tyr Lys Val Phe
 1 5 10 15
 Leu Gly Gln Leu Pro Gln Ile Lys Leu Lys Gln Lys Ala Leu Ile Ile
 20 25 30 35
 Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr Leu Gln Arg
 40 45 50 55
 Leu Asn Ala Leu Gln Val Arg Val Cys Val Ile Gln Ser Gly Gln Lys
 60 65 70 75
 Tyr Lys Asn Phe His Ser Leu Gln Arg Ile Leu Asn Asn Ala Phe Gln
 80 85 90 95
 Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu Gln Gly Val
 100 105 110
 Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr Phe Arg Gly Ile
 115 120 125 130 135 140 145 150
 Asp Phe Ile Asn Ile Pro Tyr Asp Phe Thr Arg Ser Ser Gly Cys Gln

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115 120 125
Arg Gly Gln Asn Arg Asp Gln His Ala Leu Trp Gln Pro Asn
130 135 140
Arg Ile Val Pro Ala
145 150

(2) INFORMATION FOR SEQ ID NO:734:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature
(B) LOCATION 1...227

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:734

Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
1 5 10 15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Gln Cys
20 25
Gln Ile Thr Ser Asn Lys Pro Leu Gln Leu Val Phe Cys Gln Asn
30 35 40 45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Gln Asn
50 55 60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Gln Leu Ala Pro Cys Val Leu
65 70 75 80
Asp Ala Gly Val Phe Tyr His Lys Gln Val Leu Gln Ala Leu Gln Lys
85 90 95
Gln Val Ile Leu Thr Pro His Pro Lys Gln Phe Leu Ser Leu Leu Lys
100 105 110
Ser Val Gly Ile Asn Ile Ser Met Leu Gln Leu Leu Asp Asn Lys Leu
115 120 125
Gln Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
130 135 140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
145 150 155
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
160 165 170 175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
180 185 190 195
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
200 205
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Gln Lys Unk
210 215 220 225
Lys Arg Leu

(2) INFORMATION FOR SEQ ID NO:734:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:735

(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(ix) FEATURE:

(vi) ORIGINAL SOURCE: Helicobacter pylori

(vii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:735:

Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
1 5 10 15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Gln Cys
20 25 30
Gln Ile Thr Ser Asn Asn Lys Pro Leu Gln Leu Val Phe Cys Gln Asn
35 40 45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Gln Asn
50 55 60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Gln Leu Ala Pro Cys Val Leu
65 70 75
Asp Ala Gly Val Phe Tyr His Lys Gln Val Leu Gln Ala Leu Gln Lys
80 85 90
Gln Val Ile Leu Thr Pro His Pro Lys Gln Phe Leu Ser Leu Lys
95 100 105
Ser Val Gly Ile Asn Ile Ser Met Leu Gln Leu Asp Asn Lys Leu
110 115 120
Gln Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
125 130 135
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
140 145 150
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
155 160 165
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
170 175 180
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
185 190 195
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Gln Lys Unk
200 205 210
Lys Arg Leu
215 220 225

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:734

(A) NAME/KEY: misc_feature
(B) LOCATION 1...227

(ix) FEATURE:

(vi) ORIGINAL SOURCE: Helicobacter pylori

(vii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

Met Arg Ile Leu His Tyr Gly Gly Gly Leu Pro Cys Asp Cys Pro Lys
 1
 Arg Ile Ala Gly Leu Asp Phe Ala Leu Lys Ile Leu Thr Asn Ile Thr
 20
 Ser Asp His Leu Asp Phe His Gln Asn Ile Gln Asn Tyr Arg Asp Ala
 35
 Lys Asn Ser Phe Phe Lys Asp Gly Leu Lys Val Ile Asn Arg Asp
 50
 Gln Thr Asn Ala Leu Phe Asn Pro Ile Asn Ala Arg Thr Tyr Ala Leu
 65
 Asp Lys Lys Ala His Leu Asn Val Gln Ala Phe Ser Leu Asn Pro Ser
 85
 Ile Ser Ala Ser Leu Cys Tyr Gln His Asp Leu Arg Asp Pro Asn Leu
 100
 Lys Gln Thr Ala Leu Ile His Ser Pro Leu Leu Gly Arg Tyr Asn Leu
 115
 Tyr Asn Ile Leu Ala Gly Val Leu Gly Val Lys Leu Thr Gln Leu
 130
 Pro Leu Gln Thr Ile Ala Pro Leu Leu Gln Asn Phe Tyr Gly Val Lys
 145
 Gly Arg Leu Gln Ile Val His Ser Lys Pro Leu Val Val Val Asp Phe
 160
 Ala His Thr Thr Asp Gly Met Gln Gln Val Phe
 180
 185

(2) INFORMATION FOR SEQ ID NO:736:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:736

Val Ser Ile Lys Gln Ser Gln Thr Leu Ala Asp Ile Thr Phe Gln
 1
 Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly Thr Ala
 20
 Gln Thr Gln Ala Thr Gln Phe Leu Gln Ile Tyr Asn Leu Val Val
 35
 Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn Asp Leu
 50
 Ile Tyr Lys Ser Gln Lys Phe Asp Ala Val Ile Leu Lys Ile
 65
 Lys Gln Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr Ala Ser
 85
 Ile Gln Lys Ser Gln Thr Leu His Ala Leu Leu Lys Lys Gln Arg Ile
 100
 Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Gln Ala Gln Ile
 115
 Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr Asn Met
 130
 135
 140

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:738:

Val Val Ala Asp Gln Val Arg Lys Leu Ala Gln Lys Thr Gln Lys Ala
 1 5 10 15 20 25 30
 Thr Lys Gln Ile Ala Val Val Val Lys Ser Met Gln Gln Ala Asn
 35 40 45 50 55 60
 Lys Gln Asp Val Gln Gln Lys Ser Thr Val Lys Asn Asn Met Ile
 65 70 75 80
 Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg Val
 85 90 95
 Phe Cys Gln Unk Ala Lys Leu Asp His Val Val Phe Lys Asn Asn Leu
 100 105 110
 Tyr Gln Met Val Unk Leu Val Ser Ile Pro Leu Thr Leu Pro Ala His
 115 120 125
 Lys Ser Unk Arg Leu Gln Lys Tyr Tyr Gln Gln Ala Gln Lys Gln
 130 135 140
 Asn Phe Ala Asn Thr Ser Gln Tyr Arg Ala Leu Gln Ser His His Ala
 145 150 155 160
 Ser Val His Ala Gln Ala Asn Asp Leu Val Lys Ala Val Gln Gln Asp
 165 170 175 180
 His Val Thr Asp Ser Lys Tyr Leu Gln His Lys Val His Leu Met Gln
 185 190 195
 Asp Ser Ala Lys His Val Lys Gln Asn Ile Asp Lys Met Phe Tyr Gln
 200 205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...208

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:737:

Ala Gln Arg Gln Val Asp Ile Lys Leu Thr Asp Gln Val Lys Gln Leu
 145 150 155 160
 Gln Gln Leu Tyr Ile Ile Gln Thr Gln Arg His Gln Ser Arg Arg Ile
 165 170 175 180
 Asp Asn Gln Leu Arg Gln Arg Ser Gln Arg Gln Gln Asp Pro Gln Val
 185 190 195
 Ser Gln Phe Tyr Leu Ser

615

((1)) MOLECULE TYPE: protein

((11)) HYPOTHETICAL: YES

((1)) ORIGINAL SOURCE:

((A)) ORGANISM: Helicobacter pylori

((1x)) FEATURE:

((A)) NAME/KEY: misc-feature

((B)) LOCATION 1...201

((1x)) SEQUENCE DESCRIPTION: SEQ ID NO:738

Met Asn Thr Ser Lys Lys Leu Gly Asn Pro Leu Leu Phe Leu His Asp
1 5 10 15
Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser Met Gly Gly Trp Ala
20 25 30
Thr Ser Lys Ile Tyr Gln Phe Gln Ser Ala Leu Gln Pro Ile His Phe
35 40 45
Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe Leu Asn Leu Ser His
50 55 60
Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp Gly Gly Phe Met Leu
65 70 75
Pro Leu Tyr His Gln Leu Ala Thr Gln Tyr Pro Leu Leu Lys Phe
80 85 90
Asp Gln Gln Asn Asn Pro Arg Gln Leu Leu Arg Pro Asn Thr Leu Asn
95 100 105
His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys Asp Cys Ala Val Met
110 115 120
Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu Met Leu Gln Thr Cys
125 130 135
Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser Thr Asn Leu Lys Asn
140 145 150
Leu Asp Asp Ser Leu Asn Leu Leu Asn Leu Asn Gly Ile Leu Tyr Leu
155 160 165
Leu His Asn Pro Ser Asp Leu Ser Leu Arg Arg Lys Gln Leu Trp Leu
170 175 180
Ser Lys Leu Gln Asn Gln Leu Ile
185 190 195 200

((2)) INFORMATION FOR SEQ ID NO:739:

((1)) SEQUENCE CHARACTERISTICS:

((A)) LENGTH: 127 amino acids

((B)) TYPE: amino acid

((D)) TOPOLOGY: linear

((11)) MOLECULE TYPE: protein

((11)) HYPOTHETICAL: YES

((1)) ORIGINAL SOURCE:

((A)) ORGANISM: Helicobacter pylori

((1x)) FEATURE:

((A)) NAME/KEY: misc-feature

((B)) LOCATION 1...127

((1x)) SEQUENCE DESCRIPTION: SEQ ID NO:739

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15
Phe Cys Leu Pro Val Phe Ala His Pro Gln Thr Leu Val Lys Val Lys
20 25 30

SUBSTITUTE SHEET (RULE 26)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:741

(A) NAME/KEY: misc_feature
(B) LOCATION 1...49

(ix) FEATURE:

(vi) ORIGINAL SOURCE: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:741:

Val Asn Val Gly Val Pro Phe Ser Tyr Gln Val Ser Ala Thr Phe Gln
1 5 10 15
Asn Ser Arg Leu Ser Ser Leu Leu Gln Thr Leu Lys Ser Phe Leu
20 25 30
Gln Lys Pro Leu Ile Gln Ser Ser Ala Asn Lys Ile Ala Asp Ile Phe
35 40 45
Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser Phe Leu Leu Trp Gln
50 55 60
Phe Gly Leu Gly Gly Asn Phe Gln Lys Ser Phe Asn Gly Val Tyr
65 70 75

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:740

(A) NAME/KEY: misc_feature
(B) LOCATION 1...79

(ix) FEATURE:

(vi) ORIGINAL SOURCE: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:740:

Asp Ala Gln Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Gln Leu Asp
35 40 45
Leu Asn Ser Gly Lys Ile Leu Gln Ser Phe Arg Pro Gln Arg Phe
50 55 60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65 70 75 80
Arg Ile Asp Ala Gly Gln Gln Gln Gln Gly Arg Arg Ile His Tyr Ser
85 90 95
Gln Asn Asp Leu Val Gln Tyr Ser Pro Val Thr Gln Lys His Leu Thr
100 105 110
Asp Gly Met Thr Val Arg Gln Leu Ser Arg Trp Cys His Asn His
115 120 125

617

Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys
1
Val Gly Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile
20
Gln Asn Arg Ser Tyr Leu Met Ser Ser Tyr Gln Leu Ser Phe Leu Arg
35
Asn
40

(2) INFORMATION FOR SEQ ID NO:742:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742

Met Val Gln Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe
1
Lys Asn Ala Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr
20
Lys Gln Asn Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln
35
Gln Asp Val Leu Asn Ala Leu Lys Thr Ile Tyr Pro Asn Phe Gln
50
Lys Asp Ile Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp
65
Asn Gln Leu Gly Leu Leu Ile Gln Ile Pro Ser Ser Ser Gln Thr
80
Ser Ala Ile Leu Arg Gln Asn Ile Ser Lys Ala Met Gln Gln Lys Gly
95
Val Lys Ala Leu Asn Leu Asp Ile Lys Thr Pro Lys Pro Gln Ala
110
Pro Lys Pro Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val
125
Lys Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln
140
Met Ile Ser Ser Gly Lys Gly Val Gly Lys Ser Thr Thr Ser Val
155
Asn Leu Ser Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu
170
Asp Ala Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln
185
Asn Ala Asp Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu
195
Lys Ala Phe Gly Val Ser Val Met Ser Met Gly Leu Tyr Asp Gln
210
Gly Gln Ser Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Gln
225
Gln Met Leu Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val
240
Asp Met Pro Pro Arg Asn Arg Cys Ala Ala His Ala Ala Gln Ala
255
260
265
270

618

Val Pro Leu Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser
 275 280 285
 Leu Asp Asp Ala Lys Arg Ser Leu Asp Met Phe Lys Leu His Ile
 290 295 300
 Pro Ile Ala Gly Ile Val Gln Asn Met Gly Ser Phe Val Cys Gln His
 305 310 315
 Cys Lys Lys Lys Gln Ser Gln Ile Phe Gly Ser Asn Ser Met Ser Gly Leu
 325 330 335
 Leu Gln Ala Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Gln Pro
 340 345 350
 Lys Val Arg Leu Gly Gly Asp Lys Gly Gln Pro Ile Val Ile Ser His
 355 360 365
 Pro Thr Ser Val Ser Ala Lys Ile Phe Gln Lys Met Ala Lys Asp Leu
 370 375 380
 Ser Ala Phe Leu Asp Lys Val Gln Arg Gln Lys Leu Ala Asp Asn Lys
 385 390 395 400
 Asp Ile Gln Pro Thr Gln Thr His Ala Tyr Ser His
 405 410

(2) INFORMATION FOR SEQ ID NO:743:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743

Met Gly Val Val Ile Gly Gln Thr Thr Gln Ile Gly Asp Asp Val Thr
 1 5 10 15
 Ile Tyr His Gly Val Thr Leu Gly Thr Gly Lys Phe Lys Gly Lys
 20 25 30
 Arg His Pro Thr Leu Gly Asn Arg Val Val Gly Ala Gly Ala Lys
 35 40 45
 Val Leu Gly Ala Ile Cys Val Gly Asp Asp Val Arg Ile Gly Ala Asn
 50 55 60
 Ala Val Val Leu Ser Asp Leu Pro Thr Gly Ser Thr Ala Val Gly Ala
 65 70 75 80
 Lys Ala Lys Thr Ile Thr Lys Asp Arg
 85

(2) INFORMATION FOR SEQ ID NO:744:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744

Met Leu Ser Phe Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg
1 5 10 15
Leu Leu Thr Ala Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp
20 25 30
Leu Gly Ile Gln Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys
35 40 45
Ile Gln Ala Leu Gln Gln Ile Asp Ala Leu Asp Ser Gln Gln Lys
50 55
Val Val Ser Lys Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn
60 65
Ala Asn Val Ser Asp Phe Arg Leu Asp Ser Thr Leu Met Gln Asn
70 75 80
Met Ser Leu Gly Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Leu
85 90 95
Thr Gln Ser Lys Met Ile Asn Leu Gln Lys Gln Lys Ile Leu Gln
100 105 110
Leu Lys Lys Thr Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly
115 120 125
Leu Lys Lys Thr Lys Gln Gln Gln Gln Ile Gln Leu Asn Thr Ala
130 135 140
Ile Gln Asn Tyr Lys Asn Gln Gln Gln Ile Gln Leu Asn Thr Ala
145 150 155
Ile Lys Asn Leu Gln Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser
160 165 170 175
Pro Asp Leu Ile Gln Ile Asp Lys Leu Gln Asn Leu Lys Ile Ala Asn
180 185 190

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1 5 10
Leu Val Gln Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Ser
15 20 25
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
30 35 40 45
Ser Phe Phe Ile Leu Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
50 55 60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Thr Phe Asp Leu
65 70 75 80

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Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
 Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
 85 90 95
 100 105

(2) INFORMATION FOR SEQ ID NO:745:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
 1 5 10 15
 Leu Val Gln Met Leu Ile Gly Asn Leu Gly Lys Asp Val Val Ser
 20 25 30
 Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Tyr Pro Phe Thr
 35 40 45
 Ser Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
 50 55 60
 Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
 65 70 75 80
 Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
 85 90 95
 Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:746:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746

Val Pro Ala Val Gly Gly Ala Leu Ile Trp Unk Unk Ile Unk Ile Tyr
 1 5 10 15
 Gln Leu Tyr His Gly Unk Val Asn Gln Unk Ile Phe Unk Val Leu Tyr

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SUBSTITUTE SHEET (RULE 26)

(1x) FEATURE:
(v1) ORIGINAL SOURCE: Helicobacter pylori
(111) HYPOTHETICAL: YES
(11) MOLECULE TYPE: protein
(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 118 amino acids
(1) SEQUENCE CHARACTERISTICS:
(2) INFORMATION FOR SEQ ID NO:750:
Val Ala Gly Ser Phe Ile Ala Leu Phe Ser Val Leu Ala Asp Gln
1
Phe Val Ser Val Phe Gln His Gln Asn Ala Leu Gln Arg Leu Phe Ser
20
Gln Asn Ala Thr Gln Lys Gln Lys Lys Ser Leu Cys
35
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45

(1x) FEATURE:
(v1) ORIGINAL SOURCE: Helicobacter pylori
(111) HYPOTHETICAL: YES
(11) MOLECULE TYPE: protein
(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 45 amino acids
(1) SEQUENCE CHARACTERISTICS:
(2) INFORMATION FOR SEQ ID NO:749:
Met Asp Gln Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile
1
Ala His Arg Leu Ser Thr Ile Gln Arg Cys Gln Val Ile Ile Asp Met
20
Ser Gln His Lys Asp Asn Leu Gly
35
40

(1x) FEATURE:
(v1) ORIGINAL SOURCE: Helicobacter pylori
(111) HYPOTHETICAL: YES
(11) MOLECULE TYPE: protein
(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 40
(1) SEQUENCE CHARACTERISTICS:
(2) INFORMATION FOR SEQ ID NO:748:
Met Asp Gln Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile
1
Ala His Arg Leu Ser Thr Ile Gln Arg Cys Gln Val Ile Ile Asp Met
20
Ser Gln His Lys Asp Asn Leu Gly
35
40

(A) NAME/KEY: misc-feature
(B) LOCATION 1...118

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:750

Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala
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Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr
Val Lys Ile Phe Lys Ile Asp Leu Ser Gln Phe Gln Pro Leu Gln Asn
35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115
Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Gln Arg
Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu
65 70 75 80 85 90 95 100 105 110 115
Ile Thr Gln Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys
Gly Met Pro Tyr Lys Ala His Gln Leu Val Gly Gln Ile Asn Pro Leu
115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 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7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000 10005 10010 10015 10020 10025 10030 10035 10040 10045 10050 10055 10060 10065 10070 10075 10080 10085 10090 10095 10100 10105 10110 10115 10120 10125 10130 10135 10140 10145 10150 10155 10160 10165 10170 10175 10180 10185 10190 10195 10200 10205 10210 10215 10220 10225 10230 10235 10240 10245 10250 10255 10260 10265 10270 10275 10280 10285 10290 10295 10300 10305 10310 10315 10320 10325 10330 10335 10340 10345 10350 10355 10360 10365 10370 10375 10380 10385 10390 10395 10400 10405 10410 10415 10420 10425 10430 10435 10440 10445 10450 10455 10460 10465 10470 10475 10480 10485 10490 10495 10500 10505 10510 10515 10520 10525 10530 10535 10540 10545 10550 10555 10560 10565 10570 10575 10580 10585 10590 10595 10600 10605 10610 10615 10620 10625 10630 10635 10640 10645 10650 10655 10660 10665 10670 10675 10680 10685 10690 10695 10700 10705 10710 10715 10720 10725 10730 10735 10740 10745 10750 10755 10760 10765 10770 10775 10780 10785 10790 10795 10800 10805 10810 10815 10820 10825 10830 10835 10840 10845 10850 10855 10860 10865 10870 10875 10880 10885 10890 10895 10900 10905 10910 10915 10920 10925 10930 10935 10940 10945 10950 10955 10960 10965 10970 10975 10980 10985 10990 10995 11000 11005 11010 11015 11020 11025 11030 11035 11040 11045 11050 11055 11060 11065 11070 11075 11080 11085 11090 11095 11100 11105 11110 11115 11120 11125 11130 11135 11140 11145 11150 11155 11160 11165 11170 11175 11180 11185 11190 11195 11200 11205 11210 11215 11220 11225 11230 11235 11240 11245 11250 11255 11260 11265 11270 11275 11280 11285 11290 11295 11300 11305 11310 11315 11320 11325 11330 11335 11340 11345 11350 11355 11360 11365 11370 11375 11380 11385 11390 11395 11400 11405 11410 11415 11420 11425 11430 11435 11440 11445 11450 11455 11460 11465 11470 11475 11480 11485 11490 11495 11500 11505 11510 11515 11520 11525 11530 11535 11540 11545 11550 11555 11560 11565 11570 11575 11580 11585 11590 11595 11600 11605 11610 11615 11620 11625 11630 11635 11640 11645 11650 11655 11660 11665 11670 11675 11680 11685 11690 11695 11700 11705

Thr Leu Ile Leu Asp Gly Lys Tyr Arg Tyr Leu Leu Gln Lys Asn
Gly Ala Tyr Gln Leu Lys Lys
180 195 200

(2) INFORMATION FOR SEQ ID NO:752:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752

Met Gly Gly Phe Thr Ser Ile Trp Val Ile Val Leu Val
1 5 10 15
Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Gln Leu Ala Lys Gly
20 25 30
Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Gln
35 40 45
Gln Gln Ala Lys Asn Gln Leu Lys Thr Leu Asp Ala Gln Ala Thr Gln
50 55 60
Thr Lys Val His Gln Thr Ser Gln Ile Lys Ser Lys Gln Gln Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:753:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1 5 10 15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
20 25 30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
35 40 45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Gln Thr Asn Gln Val Ala

SUBSTITUTE SHEET (RULE 26)

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:754

(A) NAME/KEY: misc-feature
(B) LOCATION 1...145

(1X) FEATURE:

(V1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 145 amino acids
(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:754:

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
Leu Leu Val Gly Cys Ser Pro His Ile Ile Gly Thr Asn Gly Val Ala
Leu Lys Leu Asn Tyr His Pro Ala Ser Gly Lys Val Gly Ala Leu Asp
Gln Lys Ile Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
Cys

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:753

(A) NAME/KEY: misc-feature
(B) LOCATION 1...97

(1X) FEATURE:

(V1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 97 amino acids
(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:753:

Leu Lys Leu Asn Tyr His Pro Ala Ser Gly Lys Val Gly Ala Leu Asp
65 70 75 80 85 90 95
Gln Lys Ile Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
Cys

625

Leu Ser Gln Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
 1 5 10 15
 Gly Gly Ala Thr Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
 20 25 30
 Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
 35 40 45
 Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
 50 55 60
 Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
 65 70 75 80
 Pro Ile Gly Tyr Val Ala Ile Ala Gln Lys Arg Leu Cys Thr Asn Gln
 85 90 95
 Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Gln Phe Leu
 100 105 110
 Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
 115 120 125
 Gly Thr Thr Phe Lys Gln Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
 130 135 140
 Ser 145

(2) INFORMATION FOR SEQ ID NO:754:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:754

Leu Ser Gln Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
 1 5 10 15
 Gly Gly Ala Thr Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
 20 25 30
 Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
 35 40 45
 Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
 50 55 60
 Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
 65 70 75 80
 Pro Ile Gly Tyr Val Ala Ile Ala Gln Lys Arg Leu Cys Thr Asn Gln
 85 90 95
 Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Gln Phe Leu
 100 105 110
 Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
 115 120 125
 Gly Thr Thr Phe Lys Gln Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
 130 135 140
 Ser 145

(2) INFORMATION FOR SEQ ID NO:755:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...98

(2) INFORMATION FOR SEQ ID NO:756:

Val Arg Leu Asn Ala Val Val Val Asp Gly Lys Tyr Lys Ile Ala
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205
 Leu Leu Ile Lys Asp Gln Ile Ser Ser Asp Ser Ala Lys Gly
 Arg Gly Thr Leu Lys Gln Arg Pro Asp Gln Ile Ala Thr Leu Phe Lys
 Ser Phe Ser Gln Gln Val Arg Tyr Gln Ile Ile Leu Gln Lys Ile
 Leu Gly Asp Leu Arg Lys Val Gln Asp Gln Leu Gly Leu Asn Ala
 Lys Ser Met Phe Gln Gln Met Asn Gln Gln Asp Gln Leu Asn Lys
 Phe Ser Gln Arg Met Leu Gln Val Val Pro Asp Gln Asp Lys Gln Val
 Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val Ile Val Pro
 Lys Thr Gln Lys Ile Leu Gly Leu Phe Met Phe Leu Ile Lys Val Tyr
 Met Val Pro Met Ile Asp Asn Ala Thr Leu Ser Gln Lys Ile Ile Tyr
 Gln Asn Arg Gly Asp Val Ala Val Ser Asn Phe Gln Phe Asn Pro
 Unk Unk Lys Lys Ile Asn Unk Leu Val Lys Gln Ala Ile Gly Asp Asn
 Leu Gln Asp Gly Ala Asn Ala Leu Gln Tyr Gln Pro Leu Ser Asp Gln

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:755

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...206

SUBSTITUTE SHEET (RULE 26)

Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe Leu
1 5 10 15
Trp Ala Asn Gln Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu Thr
20 25 30 35 40 45
Gln Lys Ser Val Ala Phe Ile Gln Gly Val Ser Lys Gln Leu Tyr Leu
50 55 60 65 70 75
Pro Ile Ala Leu Ala Asn Lys Gln Arg Gln Ser Tyr Gln Gln Gly
80 85 90 95
Phe Leu Lys Gln Leu Lys Pro Phe Val Val Phe Phe Tyr His
100 105 110 115
Asp Ala Gln Lys Ile Gln Leu Val Ala Asn Pro Lys Asp Leu Leu Asp
120 125 130 135
Thr Asp Lys Ile Phe Phe Gln Lys Ile Ala Pro Leu Leu Pro Thr Asn
145 150 155 160
Tyr Ser Val Ala Val Asp Ala Leu Ala Gln Lys Tyr His Val Asn Ile
165 170 175 180
Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val Val
185 190 195
Ile Tyr Ile Leu Leu Thr Leu Leu Gln Gly Ala Phe Leu Gly Leu Tyr
Phe Phe Lys Lys Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757

(A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(f) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:757:

Val Cys Phe Ile Leu Pro Phe Cys Leu Gly Val Leu Gly Thr Gln Ile
1 5 10 15
Phe Lys Gln Gln Thr Pro Arg Gln Leu Pro Ile Val Val Asp Leu
20 25 30 35 40 45
Asp Lys Thr Thr Ser His Gln Val Ala Phe Gln Leu Gly Ala Thr
50 55 60 65
Ser Ala Val Gln Ile Lys Tyr Gln Val Thr Ser Leu Ser Gln Ala Lys
70 75 80 85
Arg Phe Leu Asn Ser Ala Gln Val Tyr Gly Ala Leu Ile Leu Pro Lys
90 95
Asp Leu Gln Arg Lys Ile Lys Met Gly Arg Lys Val Unk Phe Ala Leu
Leu Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756

SUBSTITUTE SHEET (RULE 26)

1 Leu Val Gln Ile Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
5
10
15

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:758

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...148

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:758:

145 Lys Ile Leu Asn
130 Tyr Trp Leu Phe Cys Leu Val Leu Gln Val Ile Gln Lys Arg Val Gln
115 Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Gln Unk Ala Leu Ile
100 Ser Val Val Thr Ile Ala Gln Unk Phe Arg Ile Ala Gln Lys Unk
85 Ser Leu Ser Ser Asn Thr Phe Ile Ser Leu Phe Lys Gln Thr Ser Leu Ala
65 Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
50 Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
35 Gly Ala Tyr Ala Ser Gln Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
20 Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
15 Leu Val Gln Ile Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:758

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...148

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:758:

630

Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
 Gly Ala Tyr Ala Ser Gln Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
 Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
 Thr Phe Trp His Val Ile Phe Gln Ala Leu Lys Val Ala Thr Pro
 Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Gln Thr Ser Leu Ala
 Ser Val Val Thr Ile Ala Gln Unk Phe Arg Ile Ala Gln Lys Unk
 Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Gln Unk Ala Leu Ile
 Tyr Trp Leu Phe Cys Leu Val Leu Gln Val Ile Gln Lys Arg Val Gln
 Lys Ile Leu Asn
 145
 130
 115
 100
 85
 70
 65
 50
 45
 30
 20
 10
 5
 1

(2) INFORMATION FOR SEQ ID NO:759:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:759

Met Cys Ser Lys Ile Arg Asn Leu Ile Leu Cys Phe Gly Phe Ile
 Leu Ser Leu Cys Ala Gln Asn Ile Thr Lys Gln Asn Met Thr Gln
 Thr Asn Thr Thr Gln Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu
 Gln Gln Lys Arg Ala Gln Thr Leu Gln Leu Lys Gln Asn Gln Val
 Ala Lys Lys Ile
 65
 50
 35
 20
 10
 5
 1

(2) INFORMATION FOR SEQ ID NO:760:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

Val Val Ala Asp Gln Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130
Leu Ala Gln Ile Asn Ser Thr Ile Met Val Ile Val Gln Ile Asn
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Gln Arg Leu
Ser Asp Met Ser Lys Ser Val Gln Gln Thr Tyr Gln Lys Met Ser Ser
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
Ala Lys Ser Gly His Gln Ile Gln Ala Met Val Ser Asp Phe Ala Gln
Val Gln Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
Val Asn Leu Phe Lys Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

(A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(ix) FEATURE:

(A) ORGANISM: Helicobacter pylori

(vi) ORIGINAL SOURCE:

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 134 amino acids

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:760:

Val Val Ala Asp Gln Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130
Leu Ala Gln Ile Asn Ser Thr Ile Met Val Ile Val Gln Ile Asn
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Gln Arg Leu
Ser Asp Met Ser Lys Ser Val Gln Gln Thr Tyr Gln Lys Met Ser Ser
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
Ala Lys Ser Gly His Gln Ile Gln Ala Met Val Ser Asp Phe Ala Gln
Val Gln Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
Val Asn Leu Phe Lys Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

(A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Gln Leu Ile Leu Leu
1 5 10 15
Asp Gln Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln
20 25 30
Asp Leu Ile Lys Gln Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met
35 40 45
Val Thr His Asp Gln Asn Gln Ala Gln Lys Leu Ala Thr Lys Thr Leu
50 55 60
Gln Ile Lys Ala Leu Lys Gln Gln

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:762

(A) NAME/KEY: misc-feature
(B) LOCATION 1...73

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:762:

Val Leu Lys Thr Leu Ser Ile Arg Leu Val Ile Leu Leu Asn Cys Ser
1 5 10 15
Leu Ala Thr Asn Ala Cys Ser Gly Val Gln Lys Leu Arg Asp Gln Ser
20 25 30
His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr Lys Leu Lys Asn Met
35 40 45
Lys Gln Ile Ala Leu Leu Lys Gln Lys Gly Ile Gly Gln Ala Ser Val
50 55 60
Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Gln Ala Ile Gln Lys Ala
65 70 75
Ser Asp Gln Gln Lys Asn Ala Val Leu Lys Lys Arg Lys
80 85 90

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:761

(A) NAME/KEY: misc-feature
(B) LOCATION 1...93

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:761:

(2) INFORMATION FOR SEQ ID NO:763:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...268

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:763

Val Ile Phe Ile Ala Thr Ala Asn Ile Asp Arg Ile Pro Ala Pro
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Leu Arg Asp Arg Met Gln Phe Ile Ser Val Ser Tyr Thr Pro Ser
Leu Arg Asp Arg Met Gln Phe Ile Ser Val Ser Tyr Thr Pro Ser
Gln Lys Gln Gln Ile Ala Lys Asn Tyr Leu Ile Pro Gln Gln Gln
Lys His Ala Leu Lys Pro Ser Gln Val Asp Ile Ser His Gln Cys Leu
Lys Leu Ile Ile Gln Lys Tyr Thr Arg Gln Ala Gly Val Arg Asp Leu
65 70 75 80 85 90 95
Arg Arg Gln Ile Ala Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu
Arg Asp Asn Pro His Lys Lys Lys Gly Arg Thr Lys Lys Ser Gln Asp Lys
100 105 110 115 120 125
Asp Lys Lys Gly Gly Asn Gln Gln Asn Gln Lys Arg Gly Gln Ser Lys
Asp Phe Cys Val Ser Ile Thr Pro Asp Asn Leu Lys Gln Tyr Leu Gln
130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265
Ile Gln Ala Val Lys Ile Arg Gly Lys Gly Gln Leu Lys Leu Thr Gly
Ser Leu Gly Asp Val Met Lys Gln Ser Ala Ile Ile Ala Phe Ser Val
Val Lys Val Leu Leu Asp Asn Gln Thr Leu Lys Val Pro Lys Ile Pro
Ser Gln Thr Asp Ala Gln Asn Unk Lys Lys Lys Val Leu Lys Val
Unk Asn Ala Tyr Asp Leu His Leu His Val Pro Lys Gly Leu Arg Leu
Lys Thr Ala Arg Ala Leu Gly Ser Leu Trp Arg Ala

(2) INFORMATION FOR SEQ ID NO:764:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...273

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:764

Met Gln Phe Met Lys Lys Phe Val Ala Leu Gly Leu Ser Ala Val
 1 Leu Ser Ser Ser Leu Leu Ala Gln Gly Asp Gly Val Tyr Ile Gly Thr
 20 Leu Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
 35 Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
 40 Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Gly Leu Thr Ala
 50 Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
 65 Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
 80 Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
 95 Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
 110 Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
 125 Gly Ser Asp Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
 140 Gly Ser Asp Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
 155 Gly Ile Phe Gly Val Ala Ile Gly Asn Thr Trp Lys Ser Ser
 170 Ala Ala Asn Tyr Trp Lys Gln Ile Ile Gln Ala Lys Gly Pro Asp
 185 Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
 200 Thr Ser Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Val
 215 Asn Ile Tyr Lys His Asn Gly Val Gln Phe Gly Val Arg Val Pro Leu
 230 Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
 245 Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
 260 Phe

(2) INFORMATION FOR SEQ ID NO:764:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:764

Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Ser Ala Val
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
Gly Asp Cys Thr Gly Ser Val Gly Cys Pro Gly Leu Thr Ala
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
145 Gly Ile Phe Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
Ala Ala Asn Tyr Trp Lys Gln Ile Ile Gln Ala Lys Gly Pro Asp
Val Cys Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
210 Asn Ile Tyr Lys His Asn Gly Val Gln Phe Gly Val Arg Val Pro Leu
225 Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
240 245 250 255 260 265 270
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr

(2) INFORMATION FOR SEQ ID NO:765:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...133

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:765

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Lys Pro Glu Leu Asn Ile
1 5 10 15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
20 25 30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
35 40 45
Ser Lys Thr Ala Arg Ala Thr Glu Asp Lys Val Ile Glu Ile Arg Met
50 55 60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Glu Thr Tyr Glu Tyr Unk
65 70 75 80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Tyr Asp Lys Asp
85 90 95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
100 105 110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
115 120 125
Leu Ile Thr Ser Pro 130

(2) INFORMATION FOR SEQ ID NO:765:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...133

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:765

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Lys Pro Glu Leu Asn Ile
1 5 10 15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
20 25 30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
35 40 45
Ser Lys Thr Ala Arg Ala Thr Glu Asp Lys Val Ile Glu Ile Arg Met
50 55 60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Glu Thr Tyr Glu Tyr Unk
65 70 75 80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Tyr Asp Lys Asp
85 90 95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
100 105 110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
115 120 125
Leu Ile Thr Ser Pro 130

(2) INFORMATION FOR SEQ ID NO:766:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

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(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:767:

Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70
Asn Pro Leu Unk Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
Ile Arg Ser Leu Leu Lys Pro

(1) SEQUENCE DESCRIPTION: SEQ ID NO:766

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(11) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:766:

Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70
Asn Pro Leu Unk Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
Ile Arg Ser Leu Leu Lys Pro

(1) SEQUENCE DESCRIPTION: SEQ ID NO:766

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(11) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...147

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:767

Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
 Leu Val Ala Leu Gly Leu Ser Val Ile Gly Cys Ala Met Asn
 100 105 110 115 120 125 130 135 140
 Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln
 Thr Ile Phe Gln Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Gln
 Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp
 Leu Lys Gly

(2) INFORMATION FOR SEQ ID NO:768:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:768

Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn Ala Tyr Ser
 1 5 10 15 20 25 30 35 40 45 50 55 60
 Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg Pro Phe Ile
 Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys Gly Val Leu
 Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val His Leu Val
 Gln Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn Ala Leu Lys

639

65 70 75 80
 the Pro Asn Ala Gln Val Phe Gln Ser Asp Phe Leu Asp Phe Asn Pro
 85 90 95
 Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Phe Tyr Ala Leu
 100 105 110
 Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His Gln Ser Gln
 115 120 125
 Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Cys Leu Lys Pro
 130 135 140

(2) INFORMATION FOR SEQ ID NO:769:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...47

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:769

Met Leu Ser Ala Leu Val Met Leu Pro Phe Met Gln Val Phe Tyr Tyr
 1 5 10 15
 the Asn phe pro leu trp leu Asn leu phe leu Gly Gln Thr Ile Gly
 20 25 30
 Ala Val Ile phe phe Lys Leu Asp Lys Leu Ile phe Ser Lys Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:770:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...129

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:770

Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr
 1 5 10 15
 Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Gln Ile Lys Gln
 20 25 30
 Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Unk Pro
 35 40 45

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Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Gln
 50 55 60
 Thr Ala Thr Thr Ile Asn Gln Ile Ala Lys Tyr His Gln Lys Ser
 65 70 75 80
 Asp Lys Ala Ala Leu Gly Leu Tyr Gln Leu Lys Gly Ala Thr Thr
 85 90 95
 Asn Leu Ser Leu Gln Ala Gln Gln Leu Ser Val Lys Gln Ala Met Gln
 100 105 110
 Gln Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Gln Arg Gln
 115 120 125
 Leu

(2) INFORMATION FOR SEQ ID NO:771:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...242

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:771

Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn Asp Phe Leu
 1 5 10 15
 Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu Leu Ser Leu
 20 25 30
 Ala Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser Ile Val Asn
 35 40 45
 Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr Ala His Ser
 50 55 60
 Gln Gly Phe Ala Gly Val Phe Ala Trp Val Phe Lys Ala Leu Val
 65 70 75 80
 Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu Val Ile Asn
 85 90 95
 Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser Tyr Leu His
 100 105 110
 Gln Lys Tyr Tyr Pro His Val Val Leu Gln Gln Phe Gly Ser Ile Leu
 115 120 125
 Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met Leu Leu Phe
 130 135 140
 Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile Gly Val Phe
 145 150 155 160
 Gly Val Phe Phe Ser Ile Val Pro His Phe His Phe Lys Asn Thr
 165 170 175
 Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln Ser Tyr Gln
 180 185 190
 Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe Ser Phe Phe
 195 200 205
 Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Ala Thr Leu
 210 215 220
 Leu Gln Thr Leu Lys Leu Thr His Tyr Ile Phe Ile Phe Lys Gln Lys
 225 230 235
 Gln Cys

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Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Gln Thr Ala Pro Leu
1
5
10
15
20
25
30
35
40
45
Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln Ile Ser Leu

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 773

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...143

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 773:

Met Gln Tyr Ala Asn Ala Tyr Gln His Asn Arg Val Ser
1
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
Thr Gln Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln Ala Asn Val

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 772

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...97

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 772:

642

Gln Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val Phe Leu Lys
 Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu Gly Val Gly
 Ser Leu Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser Trp Val Asn
 Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser Trp Val Asn
 Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His Phe Leu Gly
 Val Phe Arg Phe Ala Phe Leu Tyr Lys Thr Gln Ser Val Gly Leu Ala
 Ser Lys Ser Asn Ser Met Gln Arg Phe Thr Pro Phe Phe Leu Ala
 130 115 120 100 105 90 95 110 125 140

(2) INFORMATION FOR SEQ ID NO:774:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...217

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:774

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Lys
 Leu Val Lys Thr Ala Lys Gln Lys Lys Val Phe Lys Asn Val Gly Ile
 Ser Ile Met Gly Ile Ala Phe Trp Gln Ala Ile Lys Asp Ser Ile Lys
 Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
 Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
 Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
 Asp Gln Ser Lys Gln Val Ala Gln Lys Gln Ala Gln Lys Gln Ala Asn
 Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Gln Leu Gln Gln Gln
 Gln Lys Thr Gln Gln Gln Lys Thr Gln Gln Lys Thr Gln Gln Lys
 Thr Gln Gln Gln Lys Gln Lys Thr Gln Gln Gln Lys Thr Gln
 Gln Gln Lys Gln Lys Thr Ser Asn Ile Gln Thr Asn Asn Gln Ile Lys
 Val Gln Gln Gln Gln Lys Thr Gln Gln Lys Thr Gln Gln Lys Thr Asn
 Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Gln Gln Asn Cys Gln Gln
 Asn His Asn Gln Phe Ile Lys Asn
 210 195 180 165 150 145 130 115 100 85 70 60 45 30 15 10 5

(2) INFORMATION FOR SEQ ID NO:774:

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(1x) FEATURE:
(A) NAME/KEY: misc_feature

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 84 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO: 775:

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Lys
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215
Leu Val Lys Thr Ala Lys Gln Lys Val Phe Lys Asn Val Gln Ile
Ser Ile Met Gln Ile Ala Phe Trp Gln Ala Ile Lys Asp Ser Ile Lys
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
Asp Gln Ser Lys Gln Val Ala Gln Lys Gln Ala Gln Asn
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Gln Leu Gln Gln Gln
Gln Lys Thr Gln Gln Gln Lys Thr Gln Lys Thr Gln Lys Gln Lys
Thr Gln Gln Gln Lys Thr Gln Gln Gln Lys Thr Gln Lys Thr Gln
Val Gln Gln Gln Gln Lys Thr Gln Gln Lys Thr Gln Gln Lys Thr
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Gln Asn Cys Gln Gln

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 774

(B) LOCATION 1...217

(A) NAME/KEY: misc_feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 217 amino acids

(1) SEQUENCE CHARACTERISTICS:

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(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:776:

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:776

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:776:

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Ile Val
Phe Ile Asn Glu Asp Asn Ser Val Glu Ala Tyr Glu Asn Leu Glu
His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu
Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:775

(B) LOCATION 1...84

(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:776

Met Val Ile Ser Gly His Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1 5 10 15
Ile Ile Glu Ile Ser Gin Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
20 25 30
Phe Val Phe Gly Leu Ala Gly Val Gly Ser Phe Leu Phe Gly Arg
35 40 45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
50 55 60
Val Ile Cys Pro Glu Pro Leu Ala Phe Cys Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:777:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:777

Met Arg Ile Leu Ile Leu Lys Asn Lys Pro Pro Thr Leu Arg Ser Lys
1 5 10 15
Ala Leu Thr Arg Ser Trp Gly Ile Asn Phe Ser Leu Lys Asn Thr Leu
20 25 30
Ala Tyr Ala Phe Met Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile
35 40 45
Lys Leu Lys Asn Pro Asn Tyr Asn Ser Glu Ala Ala Glu Val Ala Ser
50 55 60
Glu Ile Leu Gly Lys Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp
65 70 75
Pro Arg Thr Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp
80 85 90
Val Met Val Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe
95 100 105
Gly Gly Ile Glu Leu Ala Gly Asn Ser Trp Leu Met Ala Unk Pro Ser
110 115 120 125
Phe Glu Gly Ile Leu Gly Glu Ala Leu Val Ser Arg Lys Pro Leu
130 135 140
Leu Ser Asn Phe Tyr Ser Met Trp Gly Leu Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:778:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1 5 10 15 20 25 30
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
Val Glu Ser Val Leu Glu Ser Glu Ala Thr Glu Leu Leu Glu Lys

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 778

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 778:

Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1 5 10 15 20 25 30
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
Val Glu Ser Val Leu Glu Ser Glu Ala Thr Glu Leu Leu Glu Lys
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65 70 75 80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Ala
85 90 95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Glu
100 105 110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
115 120 125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
130 135 140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Lys Ile
145 150 155
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Lys Asn Unk Asn Unk
160 165 170 175
Ile Unk Unk Leu Asn Phe Unk Phe Leu Tyr Unk
180 185 190

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 778

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

35
40
45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
Met Gly Ala Asn Thr Leu Gln Arg Phe Leu Ser Asp Gln Asn Gly Ala
65
70
75
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Gln Phe Leu Ala
80
95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Gln
100
105
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
115
120
Thr Ala Leu Asn Gln Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
130
135
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Gln Val Asn Unk Lys Ile
145
150
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Lys Asn Unk Asn Unk
165
170
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk
180
185
190

(2) INFORMATION FOR SEQ ID NO:779:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature
(B) LOCATION 1..171

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:779

Met Asn Val Lys Lys Lys Gln Lys Pro Gln Ser Gly Lys Ile Asp Arg
1
5
10
Val Asp Cys Leu Gln Lys Leu Gly Lys Gln Asn Thr Thr Phe Leu Ser
20
25
Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro Ile Pro Gly
35
40
Val Gly Val Leu Ile Gly Phe Val Gly Val Met Ser Lys Thr
50
55
Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Gln Ala Lys Leu Ala Arg
65
70
Gln Arg Arg Ile Gln Ile Gln Lys Gln Cys Arg Gln Ser Ile Arg Gln
85
90
Leu Gln Met Tyr Gln Asn Gln Phe Asn Gln Val Phe Gln Arg Tyr Phe
100
105
His Gly Thr Ile Lys Phe Phe Asn Gln Ser Phe Asp Gln Leu Gln Arg
115
120
Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val Asn Asn Lys
130
135
Ile Gln Gln Gly Met Gly Gln Leu Leu Phe Asp Asn Lys Gln Gln
145
150
Cys Trp Gln Phe Ile Thr Ser Arg Lys Gln Gly
165
170
175
180
185
190

(2) INFORMATION FOR SEQ ID NO:780:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...141

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:780

Met Trp Pro Unk Lys Leu Phe Leu Lys Pro Leu Lys Gln Thr Ser Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140
Ala Leu Val Gly Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala
Gly Leu Lys Arg Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Leu
Ile Lys Arg Tyr Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile
Thr Ala Leu Leu Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu
Ile Val Ala Met Ala Ile Met Asn Gly Met Ser Lys Gln Phe Gln Lys
Lys Leu Phe Val Met Asn Tyr Pro Leu Thr Leu Tyr Thr Ser Pro
Tyr Gly Ile Ser Gln Gln Val Val Gln Ala Leu Gln Lys Lys Phe Pro
Asn Leu Pro Phe Ser Unk Pro Ile Cys Lys Pro Lys Ala

(2) INFORMATION FOR SEQ ID NO:781:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:781

Met Val Ser Leu Leu Gly Ala Leu Lys Arg Thr Pro Cys Thr Asn Arg
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140
Phe Tyr Leu Lys Ala Leu Phe Ala Ile Phe Tyr His Ala Val Asn
Asn Phe Leu Thr Gln Cys Pro Pro His Gln Val Arg Gln Phe Phe Ser

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(1x) FEATURE:
(A) NAME/KEY: misc_feature

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 183 amino acids
(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:783:

Val His His Leu Unk Arg Leu Asp Ser Gly Ser Gln Arg Cys Ile
1 5 10 15
Gly Cys Gly Leu Cys Ile Cys Thr Ser Asn Cys Ile Arg Ile
20 25 30
Ile Thr His Lys Gly Gln Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr
35 40 45
Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Gln Val Cys
50 55 60
Pro Gln Leu Ala Ile Val Met Gly Asn Arg Phe Gln Asn Ala Ser Thr
65 70 75 80
Gln Arg Ser Gln Tyr Gly Ser Lys Ser Gln Phe Leu Thr Ser Gln Gln
85 90 95
Asp Ala Lys Asn Cys Ser His Ala Gln Phe Leu Gly Phe Gly Ala Val
100 105 110
Ser Pro Asn Tyr Asn Gln Arg Met Gln Ala Thr Pro Leu Asp Tyr Val
115 120 125
Gln Gln Pro Ser Lys Gln Ser Lys Gln Gln Phe Unk Thr Ser Pro
130 135 140 145
Gln Ser His Lys Gly Asp Gln Asn Val 150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...153

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 153 amino acids
(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:782:

Ser Arg His Ala Gln Gly Trp Lys Arg Gln Thr Leu Pro Cys Ala Leu
35 40 45 50 55 60
Ser Phe Gln Asn Ala Leu 70

(B) LOCATION 1...183

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:783

Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Ser Ser Leu Met Trp
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Leu Gln Leu Leu Lys Ala Leu Tyr Phe Lys Leu Gln Lys Leu Gln Ser
Leu Leu Leu Lys Gln Asn Leu Leu Gln Lys Asp Arg Ile
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175
Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Gln Gly Lys Ile Leu
Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Gln Ile Thr Arg
145 150 155 160 165 170 175
Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser
180 Gln Arg Lys Gly Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:784:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...67

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:784

Met Pro Gln Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe
1 5 10 15 20 25 30 35 40 45 50 55 60 65
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Ser Leu Ile Leu
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Gln His Arg Gln
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Gln Asn
Leu Leu Val

(2) INFORMATION FOR SEQ ID NO:785:

(1) SEQUENCE CHARACTERISTICS:

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(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:785:

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Gln Phe Leu Lys Gln Leu Gln
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Gly Gln Lys Arg His Asn Gln Lys Leu Thr Ser Ile Gln Tyr Lys
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250
Val Asn Tyr Asn Lys Tyr Gln Thr Thr Leu Ile Gln Asn Met
Leu Ser Lys Ile Leu Gln Arg Ser Leu Gln Met Asp Asp Gln Gln
Val Lys Gln Met Cys Asp Gln Leu Ser Ile Lys Asn Thr Asp Asn Leu
130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
Ala Asn Gln Asp Lys Lys Ser Leu Gln Ile Gln Ser Val

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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Val Phe Leu Val Gln Ser Trp Ala Leu Ser Leu Lys Ile Asp Ser Leu
1
5
10
15
Phe Ser Leu Phe Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro
20
25
30
Phe Ala Leu Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786

(A) NAME/KEY: misc-feature
(B) LOCATION 1...173

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:786:

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Gln Phe Leu Lys Gln Leu Gln
1
5
10
15
Ser Ser Asp Leu Leu Asp Leu Phe Gln Val Phe Gly Lys Asp
20
25
30
Gly Gln Lys Arg His Asn Gln Lys Leu Thr Ser Ile Gln Tyr Lys
35
40
45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Gln Arg Ile Ala Gln Gln
50
55
60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Gln
65
70
75
Gly Val Leu Tyr Lys Gln Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
80
85
90
Val Asn Tyr Asn Lys Lys Thr Gln Thr Thr Leu Ile Gln Gln Asn Met
95
100
105
Leu Ser Lys Ile Leu Gln Arg Ser Leu Gln Met Asp Asp Gln Gln
110
115
120
Val Lys Gln Met Cys Asp Gln Leu Ser Ile Lys Asn Thr Asp Asn Leu
125
130
135
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
140
145
150
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
155
160
165
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
170
175
180
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
185
190
195
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
200
205
210
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
215
220
225
Ala Asn Gln Asp Lys Lys Ser Leu Gln Ile Gln Ser Val
230
235
240
245
250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

(A) NAME/KEY: misc-feature
(B) LOCATION 1...253

(ix) FEATURE:

653

35
40
45
Tyr Gly Leu Glu Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu
50
55
Lys Val Gly Val Tyr Glu Ser Phe Asp Leu Glu Val Leu Glu Lys Phe
65
70
Leu Leu Glu Arg Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile
85
90
Arg Ser Val Leu Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Glu
100
105
Lys Val Lys Ala Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Glu
115
120
Lys Lys Glu Leu Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn
130
135
Lys Asp Arg Asn Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe
145
150
Lys Glu Leu Glu His Ala Leu Phe Glu Ala Phe Asn
165
170

(2) INFORMATION FOR SEQ ID NO:787:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...259

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:787

Met Ser Leu Ala Pro Ser Val Met Ala Gly Phe Leu Phe Cys Ala Gly
1
5
Ser Cys Ser Leu Arg Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp
20
25
Val Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu
35
40
Asp Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser
50
55
His Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys
65
70
Asn Phe Lys Ile Asp Leu Leu Arg Phe Ser Glu Asn Glu Leu Lys Arg
85
90
Ile His Glu Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu
100
105
Trp Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr
115
120
Arg Gly Lys Asp Leu Phe Tyr Pro Glu Glu Cys Leu Ile Asn Met Val
130
135
Phe Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser
145
150
Asp Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe
165
170
Ile Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu
180
185
Ile Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys
195
200
205

Thr Pro Phe Lys Asn Asp Phe Lys Gln Arg Lys Gln Met Ala Lys
 210
 215
 220
 225
 230
 235
 240
 245
 250
 255
 Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe
 Gln Leu Ser

(2) INFORMATION FOR SEQ ID NO:788:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

Leu Leu Leu Phe Ile Val Ile Thr Ser Leu Val Lys Asn Thr Ile
 1
 5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
 100
 105
 110
 115
 120
 125
 130
 135
 140
 145
 150
 155
 160
 165
 170
 175
 180
 185
 190
 195
 200
 205
 210
 215
 220
 225
 230
 235
 240
 245
 250
 255
 260
 265
 270
 Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser

655

285

280

275
Leu Pro Lys Leu Val
290

(2) INFORMATION FOR SEQ ID NO:788:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...293

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:788

Leu Leu Leu Phe Ile Val Ile Thr Ser Leu Val Lys Asn Thr Ile
1 5 10 15 20 25
Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Cys
30 35 40 45 50 55
Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly
60 65 70 75 80 85
Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
90 95 100 105 110 115
Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
120 125 130 135 140 145
Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Phe Ile Leu
150 155 160 165 170 175
Ala Ile Asn Gln Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
180 185 190 195 200 205
Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Gln Ser Trp Gly Arg Tyr
210 215 220 225 230 235
Phe Ile Leu Ala Ser Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
240 245 250 255 260 265
Thr Leu Phe Trp Arg Gln Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
270 275 280 285 290
Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser
Leu Pro Lys Leu Val

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(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...132

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 132 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:790:

Lys Lys
180 Ile Ala Gln Phe Ile Leu His Gln Lys Ser Gln Gln Asn Gln Pro Ala
165 Val Phe Ser Met Leu Ala Thr Pro Phe Ile Leu Lys Tyr Leu Gln Ser
145 Leu Asn Ile Ala Gln Asn Asp Ile His Gln Leu Ile Leu Met Val
130 Leu Gln Gln Lys Lys Gly Ile Leu Gly Phe Leu His Gln Lys Asn Ile
115 Phe Ser Phe Val Ile Phe Leu Asn Ser Gly Ser His Gln Leu Phe Asn
100 Ala Lys Thr Ala Ile Lys Thr Ala Leu Ser Leu Ala Gln Ile Gly Gln
85 Ser Phe Lys Thr Phe Ile Tyr Ala Leu Leu Arg Phe Phe Arg Asp
65 Phe Met Gln Lys Phe Phe Val Val Ile Phe Leu Ile Leu Val Met
50 Leu Ala Leu Phe Phe Ile Thr Ile Gly Met Gln Ile Asn Val Ser Phe
35 Tyr Lys Ile Asn Val Gln Gln Phe Ala Gln Leu Lys Asn Leu Phe
20 Met Ser Leu Gly Ala Phe Ile Val Gly Met Ala Ile Ser Lys Ser Arg
15 Val Ile Val Cys Ser Ala Ala Gly Leu Ser His Phe Gly Phe Ser

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:789

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...194

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 194 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:789:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:790

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val
 1
 Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Gly Leu Arg Ala
 20
 Leu Arg His Gly Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Gly Asn
 35
 Lys Gly Thr Ile Phe Leu Gly Thr Tyr Gly Arg Gly Val Gly Asp Phe
 50
 Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg
 65
 Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn
 80
 Leu Phe Leu Gly Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly
 95
 Gly Phe Leu Gly Leu Ser Val Leu Gly Met Gly Val Phe Lys
 110
 Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys
 125
 Asn Gly Cys Phe
 130

(2) INFORMATION FOR SEQ ID NO:791:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:791

Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Gly Lys Pro Leu Tyr
 1
 Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Gly Ser Met Gly Ile Leu
 20
 Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr
 35
 Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Gly His Gly Asp
 50
 Ile Tyr Ala Leu Asn Ser Lys Leu Leu Gly Leu Arg Arg Leu Lys
 65
 Val Gly Ile Val Phe Gly Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
 80
 Val Gly Ile Val Phe Gly Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
 95
 Leu Gly Asn Leu Gly Val Ala Ser Ile Leu Ala Lys Gly Ile Asn
 100
 His Ser Leu Leu Gly Ile Ala His Thr Leu Lys Gly Gly
 115
 Val Gly Gly Leu Ser Gly Gly Gly Gly Gly Gly Arg Leu Ser Ile Ala Arg
 130
 Val Leu Ser Lys Lys Pro Gly Ile Ile Ala Asp Gly Pro Thr Gly
 145
 Asn Leu Asp Thr Thr Ser Ala Asn Gly Val Ile Ser Met Leu Gly Asn
 160
 165
 170
 175

Tyr Ile Thr Gln Asn Gln Gly Ala Leu Val Leu Ala Thr His Asp Gln
 His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Gln Lys Gln Ser
 Leu Ile Lys Gln Lys
 210
 195
 200
 205

(2) INFORMATION FOR SEQ ID NO:792:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...47

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:792

Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Phe Phe Gly Leu Asn
 1
 5
 10
 15
 Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe
 20
 25
 30
 35
 Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Gln Trp Gln Lys
 40
 45

(2) INFORMATION FOR SEQ ID NO:793:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...142

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:793

Val Gln Met Ile His Thr Gln Asp Tyr Ile Lys Met Gln Ala Ala
 1
 5
 10
 15
 Thr Gln Ala Ile Lys Arg Lys Gln Ser Ile Tyr Leu Gly Met Asp
 20
 25
 30
 Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
 35
 40
 45
 Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
 50
 55
 60
 Gln Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 69 amino acids

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:794:

Val Gln Met Ile His Thr Gln Asp Tyr Ile Lys Met Gln Gln Ala Ala
1 5 10 15
Thr Gln Ala Ile Lys Arg Lys Gln Ser Ile Tyr Leu Gln Met Asp
20 25
Ile Leu Lys Asn Gln Ala Asp Ala Leu Ile Ser Ala Gln His Ser Gln
30 35 40 45
Ala Thr Met Gln Leu Ala Thr Leu Arg Leu Gln Arg Ile Lys Gln Val
50 55 60
Gln Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gln Lys Arg Pro
65 70 75 80
Ser Val Leu Leu Asp Ala Gln Ala Asn Thr Asp Cys Lys Pro Gln Tyr
85 90 95
Leu Ile Asp Phe Ala Leu Met Gln Tyr Gln Tyr Ala Lys Ser Val Leu
100 105 110
His Tyr Asp Ser Pro Lys Val Gln Leu Ser Asn Gln Gln Asp
115 120 125
Ile Lys Gln Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
130 135 140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

(B) LOCATION 1..142

(A) NAME/KEY: misc_feature

(ix) FEATURE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 142 amino acids

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:793:

65 70 75 80
Ser Val Leu Leu Asp Ala Gln Ala Asn Thr Asp Cys Lys Pro Gln Tyr
85 90 95
Leu Ile Asp Phe Ala Leu Met Gln Tyr Gln Tyr Ala Lys Ser Val Leu
100 105 110
His Tyr Asp Ser Pro Lys Val Gln Leu Ser Asn Gln Gln Asp
115 120 125
Ile Lys Gln Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
130 135 140

659

660

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794

Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu
1 5 10 15 20 25 30 35 40 45 50 55 60
Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu
Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Gln Ala Gln
Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His
Trp Asp Ser Thr Phe
65

(2) INFORMATION FOR SEQ ID NO:795:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

Met Leu Gln Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1 5 10 15 20 25 30 35 40 45 50 55 60
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Gln Arg Val Ala Ile
Val Gly Gln Ser Gly Ser Gly Lys Ser Ile Ala Asn Leu Val Met
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Ile Leu Phe Gln
Thr Asn Leu Leu Lys Gln Ser Gln Ala Phe Unk Gln His Leu Arg
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
Pro Leu His Lys Ile Gly Lys Gln Met Ser Gln Ala Tyr Phe Leu His
His Lys Asn Ala Ser Gln Val Ser Leu Asn Gln Val Leu Asn Val
Met Lys Gln Val Gln Leu Asp Gln Asn Phe Trp Asn Val Ser Leu Met
130 135 140

(2) INFORMATION FOR SEQ ID NO:795:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

Met Gln Leu Ile Leu Gln Ser Ser Ala Arg Ala Asn Leu Leu
1 5 10 15
Lys Gln His Gln Ile Lys Phe Gln Lys Ala Leu Tyr Phe Asp Gln
20 25 30
Gln Ser Leu Lys Thr Asp Pro Arg Gln Phe Val Tyr Leu Ala Cys
35 40 45
Lys Gln Lys Leu Gln Lys Ala Lys Gln Leu Leu Ala Asn Cys Ala
50 55 60
Ile Val Val Ala Asp Ser Val Ser Val Gln Asn Arg Met Gln Arg
65 70 75 80
Lys Ala Lys Asn Lys Arg Gln Ala Leu Gln Phe Leu Lys Arg Gln Asn
85 90 95

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:796

(A) NAME/KEY: misc_feature
(B) LOCATION 1...190

(IX) FEATURE:

(VI) ORIGINAL SOURCE: Helicobacter pylori

(III) HYPOTHETICAL: YES

(II) MOLECULE TYPE: protein

(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:796:

Met Leu Gln Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1 5 10 15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Gln Arg Val Ala Ile
20 25 30
Val Gln Ser Gln Ser Gln Ser Ile Ala Asn Leu Val Met
35 40 45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gln Ile Leu Phe Gln
50 55 60
Thr Thr Asn Leu Leu Lys Gln Ser Gln Ala Phe Unk Gln His Leu Arg
65 70 75 80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
85 90 95
Pro Leu His Lys Ile Gln Lys Gln Met Ser Gln Ala Tyr Phe Leu His
100 105 110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Gln Val Leu Asn Val
115 120 125
Met Lys Gln Val Gln Leu Asp Gln Asn Phe Trp Asn Val Ser Leu Met
130 135 140

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:795

(A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(IX) FEATURE:

(VI) ORIGINAL SOURCE: Helicobacter pylori

(III) HYPOTHETICAL: YES

(II) MOLECULE TYPE: protein

Gly Asn Gly Ile Gln Val Thr Cys Ser Ala Leu Ile Ser Pro Val
 100 110 120 130 140 150 160 170 180 190
 Leu Gln Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu Lys Ala Phe
 115 125 135 145 155 165 175 185 195 205
 Asp Cys Ser Gln Ile Gln Lys Tyr Leu Gln Ser Gly Leu Trp Gln Gly
 130 140 150 160 170 180 190 200 210 220
 Ser Ala Gly Cys Val Arg Leu Gln Asp Phe His Lys Pro Tyr Ile Lys
 145 155 165 175 185 195 205 215 225 235
 Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn Val Gln Gly
 160 170 180 190 200 210 220 230 240 250
 Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu Leu

(2) INFORMATION FOR SEQ ID NO:797:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...83

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:797

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
 Leu Phe Phe Ser Gln Ser Gln Ala Phe Asp Leu Gly Lys Ile Ala Lys
 Ile Lys Ala Gly Ala Gln Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
 Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Gln Thr Phe Met Thr
 Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
 Arg Tyr Gly

(2) INFORMATION FOR SEQ ID NO:797:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...83

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...135

(1x) SEQUENCE DESCRIPTION: SEQ ID NO:797

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80

Ile Lys Phe Ser Gln Ser Gln Ala Phe Asp Leu Gly Lys Ile Ala Lys
 85 90 95 100 105 110 115 120 125 130 135

Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Gln Thr Phe Met Thr
 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000 10005 10010 10015 10020 10025 10030 10035 10040 10045 10050 10055 10060 10065 10070 10075 10080 10085 10090 10095 10100 10105 10110 10115 10120 10125 10130 10135 10140 10145 10150 10155 10160 10165 10170 10175 10180 10185 10190 10195 10200 10205 10210 10215 10220 10225 10230 10235 10240 10245 10250 10255 10260 10265 10270 10275 10280 10285 10290 10295 10300 10305 10310 10315 10320 10325 10330 10335 10340 10345 10350 10355 10360 10365 10370 10375 10380 10385 10390 10395 10400 10405 10410 10415 10420 10425 10430 10435 10440 10445 10450 10455 10460 10465 10470 10475 10480 10485 10490 10495 10500 10505 10510 10515 10520 10525 10530 10535 10540 10545 10550 10555 10560 10565 10570 10575 10580 10585 10590 10595 10600 10605 10610 10615 10620 10625 10630 10635 10640 10645 10650 10655 10660 10665 10670 10675 10680 10685 10690 10695 10700 10705 10710 10715 10720 10725 10730 10735 10740 10745 10750 10755 10760 10765 10770 10775 10780 10785 10790 10795 10800 10805 10810 10815 10820 10825 10830 10835 10840 10845 10850 10855 10860 10865 10870 10875 10880 10885 10890 10895 10900 10905 10910 10915 10920 10925 10930 10935 10940 10945 10950 10955 10960 10965 10970 10975 10980 10985 10990 10995 11000 11005 11010 11015 11020 11025 11030 11035 11040 11045 11050 11055 11060 11065 11070 11075 11080 11085 11090 11095 11100 11105 11110 11115 11120 11125 11130 11135 11140 11145 11150 11155 11160 11165 11170 11175 11180 11185 11190 11195 11200 11205 11210 11215 11220 11225 11230 11235 11240 11245 11250 11255 11260 11265 11270 11275 11280 11285 11290 11295 11300 11305 11310 11315 11320 11325 11330 11335 11340 11345 11350 11355 11360 11365 11370 11375 11380 11385 11390 11395 11400 11405 11410 11415 11420 11425 11430 11435 11440 11445 11450 11455 11460 11465 11470 11475 11480 11485 11490 11495 11500 11505 11510 11515 11520 11525 11530 11535 11540 11545 11550 11555 11560 11565 11570 11575 11580 11585 11590 11595 11600 11605 11610 11615 11620 11625 11630 11635 11640 11645 11650 11655 11660 11665 11670 11675 11680 11685 11690 11695 11700 11705 11710 11715 11720 11725 11730 11735 11740 11745 11750 11755 11760 11765 11770 11775 11780 11785 11790 11795 11800 11805 118

SUBSTITUTE SHEET (RULE 26)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:800

(A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:800:

Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Cys Val Gly
1 5 10 15
Ser Thr Val Ala Lys Ile Leu Gln Gln Gln Ile Ile Lys Asp
20 25
Arg Ala Gly Val Gln Ile Lys Ile Lys Lys Ala Val Arg Asp Val
30 35
Lys Lys His Lys Gly Tyr Ala Phe Gln Ile Ser Asp Asp Leu Gln Ser
40 45
Val Ile Gln Asp Lys Gly Ile Asp Ile Val Val Gln Leu Met Gly Gly
50 55
Val Gln Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala Lys Gln Lys
60 65
Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His Arg Tyr Gln
70 75
Leu Gln Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Gln Ala Ser Val
80 85
Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly Leu Ser Ala
90 95
Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr Ser Asn Tyr
100 105
Lys Asp Ala Gln His Leu Gly Tyr Ala Gln Leu Asn Pro Gln Phe Asp
110 115
Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu Ala Ser Leu
120 125
Ala Tyr Gly Ile Asp Ala Lys Leu Gln Ile Leu Ile Gln Gly Ile
130 135
Gln Lys Ile Gln Pro Asp Asp Met Gln Phe Lys Asn Gln Ala Ser
140 145
Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys Asp Ala Leu
150 155
Lys Asp Ala Gln His Leu Gly Tyr Ala Gln Leu Asn Pro Gln Phe Asp
160 165
Lys Asp Ala Gln His Leu Gly Tyr Ala Gln Leu Asn Pro Gln Phe Asp
170 175
Lys Asp Ala Gln His Leu Gly Tyr Ala Gln Leu Asn Pro Gln Phe Asp
180 185
Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu Ala Ser Leu
190 195
Ala Tyr Gly Ile Asp Ala Lys Leu Gln Ile Leu Ile Gln Gly Ile
200 205
Gln Lys Ile Gln Pro Asp Asp Met Gln Phe Ala Lys Gln Phe Gly Tyr
210 215
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gln Gly Leu His
220 225
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gln Gly Leu His
230 235
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gln Gly Leu His
240 245
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gln Gly Leu His
250 255

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:799

(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

Met Leu Gly Lys Lys Asn Gln Val Leu Ile Asp Gln Asn Leu Val
1 5 10 15
Ile Lys Gln Ile Gln Ser Gly Phe Ile Asp Ala Leu Phe Ser Lys Ile
20 25 30
Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala Leu Asp
35 40 45
Gln Lys Thr Asp Ala Ile Leu Asp Lys Ala Leu Ser Met Val Leu Asn Val Ala
50 55 60
Ala Val Thr Ser Ile Val Met Met Pro Leu Lys Lys Thr Asp Ile
70 75
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Gln Phe Lys Ile Val Lys
80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801

(A) NAME/KEY: misc_feature
(B) LOCATION 1...252

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:801:

Met Gln Gln Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile Ala Ser Trp
1 5 10 15
Ile Lys Gln Ile Gln Ser Gly Phe Ile Asp Ala Leu Phe Ser Lys Ile
20 25 30
Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala Leu Asp
35 40 45
Gln Lys Thr Asp Ala Ile Leu Asp Lys Ala Leu Asn Leu Cys Ala
50 55 60
Ile Val Gln Met Ile Gln Thr Ala Ser Leu Leu His Asp Asp Val Ile
65 70 75
Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn Ala Leu Phe
80 85 90
Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr Ser Lys Ala
95 100 105
Phe Phe Gln Leu Ser Lys Met Gly Gln Ser Ile Ala Gln Ala Leu Ser
110 115 120
Asn Ala Val Leu Arg Leu Ser Arg Gly Gln Ile Gln Asp Val Phe Val
125 130 135
Gly Gln Cys Phe Asn Ser Asp Lys Gln Lys Tyr Trp Arg Ile Leu Gln
140 145 150
Asp Lys Thr Ala His Phe Ile Gln Ala Ser Leu Lys Ser Met Ala Ile
155 160 165
Leu Leu Asn Lys Asp Ala Lys Met Tyr Ala Asp Phe Gly Leu His Phe
170 175 180
Gly Met Ala Phe Gln Ile Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp
185 190 195
Ala Asn Thr Leu Gly Lys Pro Asn Phe Ser Asp Phe Lys Gln Gly Lys
200 205 210
Thr Leu Pro Tyr Leu Leu Tyr Gln Lys Leu Asn Gln His Gln
215 220 225
Gln Gly Phe
230 235 240

666

Arg Ser Asp Ala Ile Val Asn Ser Glu Ala Val Val Asp Ser
 Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser
 Leu Arg Asp Arg Lys Asp Glu Leu Met Glu Tyr Cys Asp Val Ser Phe
 115 120 125
 Glu Thr Glu Ala Met Arg Met Phe Asn Glu Asn Ile Arg Glu Val
 130 135 140
 Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Glu Arg Glu
 145 150 155
 Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Ile Thr Ile
 160 165 170
 Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys
 175 180 185
 Glu Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Glu Glu
 190 200 205
 Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Glu Ile
 210 215 220
 Thr Asp Leu Glu Asn Glu Glu Thr Val Ser Glu Ile Leu Arg Lys Ile
 225 230 235
 Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
 240 245 250

(2) INFORMATION FOR SEQ ID NO:802:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...165

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:802

Met Arg Ala Ile Val Leu Ala Arg Ser Ser Lys Arg Ile
 1 5 10 15
 Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met Leu Ala Tyr
 20 25 30
 Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys Val Phe Ile
 35 40 45
 Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn Tyr Gly Ala
 50 55 60
 Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Asp Arg Ala Thr
 65 70 75 80
 Thr Leu Glu Val Met Ala Tyr His Met Lys Glu Leu Glu Leu Lys Asp
 85 90 95
 Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val Ser Val Phe Leu Glu Glu
 100 105 110
 Lys His Leu Glu Asn Ala Phe Glu Thr Leu Lys Glu Asn Glu Asn Thr
 115 120 125
 Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser Ala Ser Pro Ile Val Leu
 130 135 140
 Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu Leu Lys Ser Ile Glu Thr
 145 150 155 160
 Arg Ala Arg Lys Ile

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(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:804:

Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn Ala Lys Asn
1 5 10 15
Pro Lys Ser Phe Asp Asn Lys Gly Asn Thr Lys Phe Ile Ala Ile
20 25 30
Thr Ser Gly Lys Gly Val Gly Lys Ser Asn Ile Ser Ala Asn Leu
35 40 45
Ala Tyr Ser Leu Tyr Lys Gly Tyr Lys Val Gly Val Phe Asp Ala
50 55 60
Asn Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val Lys Thr Gln
65 70 75
Lys Asn Ile Leu His Asp Leu Lys Gly Gln Asp Lys Leu Lys Gln Ile
80 85 90
Ile Cys Gln Ile Gln Pro Gly Leu Cys Leu Ile Pro Gly Asp Ser Gly
95 100 105 110
Gln Gln Ile Leu Lys Tyr Ile Ser Gln Ala Gln Asp Phe Asp Ser Phe
115 120 125
Leu Asp Gln Gln Gly Val Leu Ser Ala Leu Ile Tyr Ile Leu Ile Asn
130 135 140
Thr Ser Lys Asn Leu Gly Pro Leu Ser Gln Thr Phe Leu Asn Phe
145 150 155 160
Gln Ser Phe Leu Phe Ile Phe Ile Gln Ser Pro
165 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...171

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:803:

165

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...199
 (1x) SEQUENCE DESCRIPTION: SEQ ID NO:804

Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly Lys Ser
 1 5 10 15 20 25 30 35 40 45 50
 Leu Ala Gln Gln Leu Gly Leu Ala Leu Lys Leu Gln Val Leu Asp Thr
 Asp Met Ile Ile Ser Gln Arg Val Gly Leu Ser Val Arg Gly Ile Phe
 Gln Gln Leu Gly Asp Asn Phe Arg Met Phe Gln Lys Ile
 55 60

(2) INFORMATION FOR SEQ ID NO:805:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...199

(1x) SEQUENCE DESCRIPTION: SEQ ID NO:805

Met Ser Ile Lys Gln Asn Leu Gln Val Arg Asn Gln Phe Lys Ser
 1 5 10 15 20 25 30 35 40 45 50
 Asp Gln Lys Leu Leu Gln Gly Ala Phe Arg Leu Gln Lys Phe Lys
 Arg Tyr Lys Trp Val Leu Phe Ile Val Val Ala Phe Ile Ala Tyr
 Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Gln Thr Arg Gln
 Arg Ile Thr Gln Ile Tyr Asn Gln Val Leu Gln Ser Pro Asn Asn Ile
 55 60 65 70 75 80
 Ala Leu Gln Lys Arg Leu Lys Gln Val Ala Pro Gln Leu Tyr Asp Leu
 85 90 95
 Tyr Gln Phe Ala Arg Ala Ser Gln Arg Asn Asp Ala Asn Gln Phe Lys
 100 105 110
 Arg Leu Ser Gln Ser Ser Asn Gln Ile Val Lys Ala Phe Ala Lys Tyr
 115 120 125
 Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Gln Lys Ser Pro
 130 135 140
 Ile Leu Lys Gln Met Ser Ala Leu Gln Gln Val Asn Leu Leu Tyr Gln
 145 150 155
 Gln Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser Thr
 160 165 170 175
 Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys His
 180 185 190
 Tyr Gly Met Leu Gln Asp Ile 195

(2) INFORMATION FOR SEQ ID NO:806:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...130

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 806

Met Asp Ala Leu Gln Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1 5 10 15
Thr Pro Lys Gln Cys Gly Ile Phe Gln Tyr Ile Lys Ser Leu Phe Pro
20 25 30
Ala Phe Lys Thr Leu Gln Cys Gln Lys Asn Gly Val Lys Asn Leu Phe
35 40 45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Gln Lys Gln His
50 55 60
Ala Lys Gln Lys His Val Lys Gln Asn Val Unk Pro Leu His Phe Cys
65 70 75 80
Unk Ala Gly His Ile Unk Val Val Pro Gly Unk Unk Unk Unk Unk
85 90 95
Asp Ser Phe Unk Unk Ile Ile Lys Gln Gly Phe Leu Tyr Gly Arg Gly
100 105 110
Ala Gln Asp Met Lys Gly Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
115 120 125
Lys Phe 130

(2) INFORMATION FOR SEQ ID NO: 806:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...130

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 806

Met Asp Ala Leu Gln Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1 5 10 15
Thr Pro Lys Gln Cys Gly Ile Phe Gln Tyr Ile Lys Ser Leu Phe Pro
20 25 30
Ala Phe Lys Thr Leu Gln Cys Gln Lys Asn Gly Val Lys Asn Leu Phe
35 40 45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Gln Lys Gln His
50 55 60
Ala Lys Gln Lys His Val Lys Gln Asn Val Unk Pro Leu His Phe Cys
65 70 75 80

670

Unk Ala Gly His Ile Unk Val Val Pro Pro Gly Unk Unk Unk Unk
 Asp Ser Phe Unk Ile Ile Lys Gln Gly Phe Leu Tyr Gly Arg Gly
 Ala Gln Asp Met Lys Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
 Lys Phe 130
 115 120 125

(2) INFORMATION FOR SEQ ID NO:807:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...101

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:807

Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly Ala Ile Leu
 1 5 10 15
 Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Gln Tyr Leu Lys
 20 25 30
 Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Gln Gln Ser Ser Ile
 35 40 45
 His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala Met Gly Gly
 50 55 60
 Gly Arg Met Gly Val Leu Gln Thr Ser Phe Lys Gln Cys Gln Ser
 65 70 75 80
 Asp Leu Phe Gly Gln Ala Val Leu Cys Gly Gly Leu Gln Val Asp
 85 90 95
 Arg Lys Asn Gly Val 100

(2) INFORMATION FOR SEQ ID NO:808:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:808

671

Met Lys Lys Phe Ser Gln Ser Leu Ala Leu Ile Ile Ser Met
 1 5 10 15
 Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val Phe Leu Gly Ala Gly
 20 25 30
 Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys
 35 40 45
 Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr
 50 55 60
 Gln Phe Phe Phe Gln Lys His Phe Gly Leu Arg Leu Tyr Gly Val Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:809:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:809

Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe Leu Ile Ile
 1 5 10 15
 Val Gly Leu Ala Val Leu Val Ala Gln Val Trp Val Thr Thr Asp
 20 25 30
 Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val Ala Ser Gln
 35 40 45
 Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr Asp Lys Gln
 50 55 60
 Phe Arg Phe Tyr Ala Arg Phe Gln Gln Ile Pro Arg Phe Val Gln
 65 70 75 80
 Ser Leu Leu Ala Val Gln Asp Thr Leu Phe Phe Gln His Gly Ile
 85 90 95
 Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala Lys Ser Gly
 100 105 110
 Arg Tyr Thr Gln Gly Ser Thr Leu Thr Gln Gln Leu Val Lys Asn
 115 120 125
 Met Val Leu Thr Arg Gln Lys Thr Leu Thr Arg Lys Leu Lys Gln Ala
 130 135 140
 Ile Ile Ser Ile Arg Ile Gln Lys Val Leu Ser Lys Gln Gln Ile Leu
 145 150 155 160
 Gln Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr Tyr Gly Val
 165 170 175
 Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp Lys Leu Thr
 180 185 190
 Leu Lys Gln Ile Thr Met Leu Val Ala Leu Pro Arg Ala Pro Ser Phe
 195 200 205
 Tyr Asp Pro Thr Lys Asn Leu Gln Phe Ser Leu Ser Arg Ala Asn Asp
 210 215 220
 Ile Leu Arg Arg Leu Tyr Ser Leu Gly Unk Ile Ser Ser Asn Gln Leu
 225 230 235 240
 Lys Ser Ala Leu Asn Gln Val Pro Ile Val Tyr Asn Gln Thr Ser Thr
 245 250 255

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Gln Asn Ile Ala Pro Tyr Val Val Asp Gln Val Leu Lys Gln Leu Asp
 260 265 270 275 280 285
 Gln Leu Asp Gln Arg Leu Ala Leu Gln Ser Leu Arg Phe Gln His
 290 295 300 305 310 315 320
 Gln Lys Ile Leu Gln Lys Ile Ala Lys Gln Lys Pro Lys Thr Asn Ala
 325 330 335 340 345 350 355
 Ser Asn Asp Lys Asp Gln Asp Asn Leu Asn Ala Ser Met Ile Val Thr
 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445
 His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ala Ile Ala Trp Leu
 Tyr Unk Arg Lys Phe Leu Gln Val Thr Leu Gln Gln Ala Leu Ser

(2) INFORMATION FOR SEQ ID NO:810:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...218

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:810

Met Asn Asp Thr Thr Gln His His Gly Ser Asn Pro Leu Asn Ala Pro
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140
 Gln Arg Ile Met Gln Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
 Gly Leu Gln His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
 Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Gln Leu
 Val Gln Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala
 Phe Gly Val Gln Ala Val Leu Phe Phe Gly Leu Gln Thr Ile Arg Ser

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(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:812:

Met Met Asp Lys Val Gly Phe Lys Ser Gln Gly Ile Phe Val Met Asp
 1 5 10 15
 Ala Ser Lys Arg Asp Gly Leu Asn Ala Tyr Phe Gly Leu Gly
 20 25 30
 Lys Asn Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly
 35 40 45
 Thr Gln Unk Leu Leu Ala Ile Leu Gly His Gln Gly His Phe Lys
 50 55 60
 Asn Lys Asp Leu Leu Lys Asn Leu Gly Ile Met Gly Gly Leu Leu Ala
 65 70 75
 Leu Val Phe Ala Leu Ile Ala His Leu Pro Leu Val Phe Gln Gly
 80 85 90
 Phe Asn Val Ser Gln Thr Pro Ala Ser Leu Ile Thr Ile Leu Leu Leu
 95 100 105
 Phe Leu Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe
 110 115 120
 Ser Arg Lys Asn Gln Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser
 125 130 135
 Ser Lys Gln Thr Leu Ala Lys Ala Leu Val Ser Ile Val Asn Gln Asn
 140 145 150
 Lys Ala Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr
 155 160 165
 His Pro Pro Leu Leu Gln Arg Leu Lys Ala Leu Asp Tyr Gln Ile Gln
 170 175 180 185 190

(11) SEQUENCE DESCRIPTION: SEQ ID NO:811

(1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1..192

(1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:811:

145 150 155 160
 Ile Tyr Gln Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
 165 170 175
 Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
 180 185 190
 Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
 195 200 205
 Phe Ala Ser Lys Lys Gln Gly Ala Gln
 210 215

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(a) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(a) NAME/KEY: misc-feature

(b) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

Met Ile Leu Ser Ile Gln Ser Ser Cys Asp Ser Ser Leu Ala Leu
1 5 10 15
Thr Arg Ile Gln Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
20 25
Gln Lys His Ser Ser Tyr Gln Val Val Pro Gln Ile Ala Ser
30 35
Arg Leu His Ala Gln Asn Leu Pro Leu Leu Gln Arg Val Lys Ile
40 45
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
50 55
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
60 65
Gln Pro Gln Leu Ser Val Thr Leu Ile Gln Lys Met Met Ala Lys
70 75
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Gln Asp His Leu
80 85
Arg Gln His Val Tyr Ser Leu Phe Ile Asn Gln Lys Gln Thr Arg Met
90 95
Pro Leu Ser Val Leu Leu Val Ser Gln Gln His Ser Leu Ile Leu Gln
100 105
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Gln Asp His Leu
110 115
Arg Gln His Val Tyr Ser Leu Phe Ile Asn Gln Lys Gln Thr Arg Met
120 125
Pro Leu Ser Val Leu Leu Val Ser Gln Gln His Ser Leu Ile Leu Gln
130 135
Ala Arg Asp Tyr Gln Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
140 145
Ser Phe Gln Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gln
150 155
Tyr Pro Gln Gln Pro Ile Val Gln Lys Leu Ala Leu Asp Tyr Ala His
160 165
Pro Asn Gln Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
170 175
Leu Ala Phe Ser Phe Ser Gln Lys Asn Ala Val Arg Leu Gln Val
180 185
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Gln Asp Lys Cys Ala
190 195
Gln Phe Asp Cys Gln Leu Val Leu Ala Pro Leu Gln Phe Cys Ser Asp
200 205
Asn Ala Met Ile Gln Arg Ser Ser Leu Gln Ala Tyr Gln Lys Lys
210 215
Arg Phe Ile Lys Ile Lys Arg Pro Lys Ile Phe Gln Ile Val Gln Gln
220 225
Tyr His Phe Gln Ser Ala Ala Ile Gln His Leu Ile Gln Gln Thr Lys
230 235
Gln Lys Asn Ala His Asn Leu Asn Asp Gln Val Lys Gln Lys Ile Gln
240 245
Tyr His Phe Gln Ser Ala Ala Ile Gln His Leu Ile Gln Gln Thr Lys
250 255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gln Ile Val Gln Gln
260 265
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Gln Asp Lys Cys Ala
270 275
Gln Phe Asp Cys Gln Leu Val Leu Ala Pro Leu Gln Phe Cys Ser Asp
280 285
Asn Ala Met Ile Gln Arg Ser Ser Leu Gln Ala Tyr Gln Lys Lys
290 295
Arg Phe Ile Pro Leu Gln Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
300 305
Lys Asn Phe Gln
310 315
320 325
330 335
340

(2) INFORMATION FOR SEQ ID NO:812:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc-feature
(B) LOCATION 1..340

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:812

Met Ile Leu Ser Ile Gln Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1 5 10 15
Thr Arg Ile Gln Asp Ala Lys Leu Ile Ala His phe Lys Ile Ser Gln
20 25 30 35
Gln Lys His Ser Ser Tyr Gln Val Val Pro Gln Ile Ala Ser
40 45 50
Arg Leu His Ala Gln Asn Leu Pro Leu Leu Gln Arg Val Lys Ile
55 60 65
Ser Leu Asn Lys Asp phe Ser Lys Ile Lys Ala Ile Thr Asn
70 75 80
Gln Pro Gln Leu Ser Val Thr Leu Ile Gln Gln Met Met Met Ala Lys
85 90 95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Gln Asp His Leu
100 105 110
Arg Gln His Val Tyr Ser Leu phe Ile Asn Gln Lys Gln Thr Arg Met
115 120 125
Pro Leu Ser Val Leu Leu Val Ser Gln Gln His Ser Leu Ile Leu Gln
130 135 140
Ala Arg Asp Tyr Gln Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
145 150 155
Ser phe Gln Ser phe Asp Lys Val Ser Lys Met Leu Asp Leu Gln
160 165 170
Tyr Pro Gln Gln Pro Ile Val Gln Lys Leu Ala Leu Asp Tyr Ala His
175 180 185
Pro Asn Gln Pro Leu Met phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
190 200 205
Leu Ala phe Ser phe Ser Gln Lys Asn Ala Val Arg Leu Gln Val
210 215 220
Gln Lys Asn Ala His Asn Leu Asn Asp Gln Val Lys Gln Lys Ile Gln
225 230 235
Tyr His phe Gln Ser Ala Ile Gln His Leu Ile Gln Gln Thr Lys
240 245 250
Arg Tyr phe Lys Ile Lys Arg Pro Lys Ile phe Gln Ile Val Gln Gln
255 260 265
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala phe Gln Asp Leu Cys Ala
270 275 280
Gln phe Asp Cys Gln Leu Val Leu Ala Pro Leu Gln phe Cys Ser Asp
285 290 295
Asn Ala Ala Met Ile Gln Arg Ser Ser Leu Gln Ala Tyr Gln Lys Lys
300 305 310 315
Arg phe Ile Pro Leu Gln Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
320 325 330 335
Lys Asn phe Gln
340

(2) INFORMATION FOR SEQ ID NO:813:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

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Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val Gly Ala Asn
1
5
10
15
Leu Ser Ala Gln Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:814

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...130

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:814:

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro
1
5
10
15
Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Gln Asn Lys Tyr Gln
20
25
30
Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Asp Lys Gln
35
40
45
Thr Asn Thr Pro Leu Phe Gln Lys Ser Pro Leu Asp Ser Ser Leu Gln
50
55
60
Leu Tyr Lys Asn Ser Gln Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr
65
70
75
Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Gln
80
85
90
Asn Leu Lys Arg Leu Val Val Ile Gln Pro Gln Ile Gln Val Ile Phe
95
100
105
Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Gln Ile Leu Gln Asn Arg
110
115
120
Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser
125
130
135
Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp
140
145
150
Leu Lys Leu Phe Asn Ala Tyr Tyr Gln Arg Tyr Ser His Gln Met Ile
155
160
165
Gln Ile Asn Gln His Phe Thr Arg Ala Leu Gln His Gly Ala Ile Ser
170
175
180
Val Gly Asn Asp Ala Lys Ala His Ser
185
190
195
200

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:813

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...201

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Gln
20 25 30
35 40 45
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val
50 55 60
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys
65 70 75 80
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu
85 90 95
Gln Leu Asn Asn Val Gln Ile Val Asn Gln Gln Ala Gln Lys Gly Ile
100 105 110
Tyr Tyr Thr Arg Val Arg Asn Gln Ser Lys Leu Val Phe Ala Gly Phe
115 120 125
Lys Gly 130

(2) INFORMATION FOR SEQ ID NO:815:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...144

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:815

Met Lys Ile Gln Thr Ile Ser Thr Leu Val Leu Thr Ile Ile Met Val
1 5 10 15
Ile Gln Lys Met Ile Val Gly Lys Ile Ser Pro His Lys Thr Ala Gln
20 25 30
Gln Phe Thr Asn Leu Met Leu Asn Met Ile Ala Val Leu Asp Ser Gln
35 40 45
Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe Gln Phe Thr Asn Ser
50 55 60
Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys Val Asn Pro Gly Thr
65 70 75 80
Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys Tyr Val Leu Asn Lys
85 90 95
Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala Asp Leu Asp Val Ile
100 105 110
Val Leu Lys Asp Ser Gly Val Val Gly Unk Unk Asn Gly Tyr Gly Asn
115 120 125
Asp Gly Gln Tyr Gly Thr Leu Gly Val Unk Ala Tyr Ala Leu Gly Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:816:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...309

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:816

Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser Tyr
1 5 10 15
Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys Lys
20 25 30
Gln Arg Phe Met Asp Gln Ile Lys Thr Leu Leu Val Asp Phe Phe Pro
35 40 45
Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe
50 55 60
Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met Lys
65 70 75 80
Leu Leu Ser Lys Lys Asp Gln Ile Leu Ala Asn Phe Val Ala Gln Val
85 90 95
Thr Phe Ile Leu Ile Thr Thr Ile Ile Ala Leu Ser Thr
100 105 110
Leu Gly Val Gln Thr Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly
115 120 125
Ile Ala Val Ala Leu Ala Leu Lys Asp Tyr Leu Ser Ile Ala Gly
130 135 140
Gly Ile Ile Leu Ile Ile Leu His Pro Phe Lys Gly Asp Ile Ile
145 150 155 160
Gln Ile Ser Gly Leu Gln Gly Lys Val Gln Ala Leu Asn Phe Phe Asn
165 170 175
Thr Ser Leu Arg Leu His Asp Gly Arg Ala Val Leu Pro Asn Arg
180 185 190
Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys Arg
195 200 205
Arg Ile Gln Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Gln Leu
210 215 220
Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Gln Lys Ile Asp
225 230 235 240
Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser
245 250 255
Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Gln Asp Gly Ile Phe
260 265 270
Asn Val Arg Ser Gln Leu Ile Gln Arg Ile Lys Asn Ala Leu Asp Ala
275 280 285
Asn Arg Ile Gln Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys
290 295 300
Gln Asp Ser Ser Lys
305

(2) INFORMATION FOR SEQ ID NO:817:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817

Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Unk Leu Lys Lys Arg
1 5 10 15
His Leu Ile Ala Leu Ser Leu Pro Leu Ser Tyr Ala Asn Gly Phe
20 25 30
Lys Ile Gln Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr
35 40 45
Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn
50 55 60
Met Gly Phe Thr Asn Asp Trp Gly Gln Asn Arg Ser Gln Phe Gln Met
65 70 75 80
Thr Thr Thr Val Ile Asn Ile Pro Thr Phe Ser Phe Lys Val Pro Thr
85 90 95
Thr Asn Gln Unk Leu Tyr Ser Val Thr Ser Leu Gln Ile Asp Lys Ser
100 105 110
Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Gly Asn Ile
115 120 125
Leu Lys Ala Leu Gly Asn Thr Ala Thr Asn Gly Leu Ser Gln Ala
130 135 140
Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val
145 150 155 160
Thr Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(f1i) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818

Met Cys Leu Ala Ile Pro Ser Lys Val Ile Ala Ile Asn Asp Asn Val
1 5 10 15
Ala Leu Leu Gln Thr Leu Gly Val Gln Arg Gln Ala Ser Leu Asp Leu
20 25 30
Met Gly Gln Ser Val Lys Val Gly Asp Tyr Val Leu Leu His Ile Gly
35 40 45
Tyr Val Met Ser Lys Asp
50

(2) INFORMATION FOR SEQ ID NO:819:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:820

(A) NAME/KEY: misc_feature
(B) LOCATION 1...168

(1x) FEATURE:

(v1) ORIGINAL SOURCE: Helicobacter pylori
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 168 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:820:

Met Lys Tyr Leu Tyr Phe Leu Ile Tyr Ala Ile Gly Leu Phe Ala
1 5 10 15
Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gly Lys Leu Pro Lys
20 25
Ile Gly Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr Ala Leu Lys
30 35 40 45
Leu His Gly Val Leu Ala Asn Asp Leu Lys Thr Ser Gly His Phe Asp
50 55
Val Ser Gly Asn Lys Gly Ala Ile Asn Tyr Ala Gly Leu Lys
60 65
Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala Val Gly Asn
70 75 80
85
Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp Thr Gly Thr
90 95
Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp Leu Tyr Pro
100 105 110
Phe Ala His Asn Met Ala Ile Val Val Asn Asp Tyr Leu Lys Ala
115 120 125
Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser Lys Tyr Ile
130 135 140
Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asn Tyr Thr Met Arg Tyr
145 150 155
Gln Lys Gln Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe Pro Lys Trp
160 165 170 175 180 185 190 195
Ala Asn Ala Gln Gln Thr Gln Phe Tyr Tyr 200

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:819

(A) NAME/KEY: misc_feature
(B) LOCATION 1...202

(1x) FEATURE:

(v1) ORIGINAL SOURCE: Helicobacter pylori
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear
(B) TYPE: amino acid
(A) LENGTH: 202 amino acids

(1) SEQUENCE CHARACTERISTICS:

681

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Gly Lys
Phe Tyr His Lys Met Arg Arg Leu Gly Lys Thr Leu Asp Gly Ser Tyr
Gln Gln Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Gln Leu Gly Arg
Leu Gln Gly Leu Ser Leu Gln Lys Ser Ala Lys Gln Asp Ser Ser Leu
65 70 75 80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Ile Gln Lys
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Ile Gln Lys
Ser Met Asp Lys Gln Arg Asp Tyr Leu Gln Lys Ile Ile Unk Unk
100 105 110 115 120 125 130 135 140 145 150 155 160
Thr Gln Lys Gln Val Leu Lys Met Tyr Gln Gln Gly Tyr Ser Val Asp
Ser Ile Ser Lys Gln Phe Lys Val Ser Lys Gly Gln Val Gln Phe Ile
Leu Asn Met Ala Gly Leu Lys Trp 165

(2) INFORMATION FOR SEQ ID NO:820:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:820

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Gly Lys
Phe Tyr His Lys Met Arg Arg Leu Gly Lys Thr Leu Asp Gly Ser Tyr
Gln Gln Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Gln Leu Gly Arg
Leu Gln Gly Leu Ser Leu Gln Lys Ser Ala Lys Gln Asp Ser Ser Leu
65 70 75 80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Ile Gln Lys
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Ile Gln Lys
Ser Met Asp Lys Gln Arg Asp Tyr Leu Gln Lys Ile Ile Unk Unk
100 105 110 115 120 125 130 135 140 145 150 155 160
Thr Gln Lys Gln Val Leu Lys Met Tyr Gln Gln Gly Tyr Ser Val Asp
Ser Ile Ser Lys Gln Phe Lys Val Ser Lys Gly Gln Val Gln Phe Ile
Leu Asn Met Ala Gly Leu Lys Trp 165

Leu Asn Met Ala Gly Leu Lys Trp
165

(2) INFORMATION FOR SEQ ID NO:821:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821

Val Val Ser Gly Val Val Ile Ile Val Phe Val Phe Val Pro Ile Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Ile Ala Ser Leu Ser Leu Phe Phe Val Gly Lys Asn Phe Met Pro
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180
Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala Phe Val Phe Leu
Ser Asp Gly Asp Val Val Leu Ser Val Gly Thr Thr Pro Ser
Ile Ser Leu Asp Gly Ser Lys Asp Leu Met Leu Asn Ile Gly Ser Ala
Ile Lys Lys His Val Lys Gly Val Lys Ser Ile Val Ala Arg Thr Gly
Ser Asp Gly Leu Asp Leu Gly Lys Leu Asn Gly Thr Asp Thr
Phe Ile Ser Phe Ile Pro Lys Lys Gly Trp

(2) INFORMATION FOR SEQ ID NO:822:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES

(2) INFORMATION FOR SEQ ID NO:823:

Leu Asp Pro Phe Ser His Lys Gln Asn Phe Leu Ala Val Gln Thr Phe
1
Lys Met Leu Gln Lys Thr Gln Ser Lys Asp Asn Leu Asn Trp Met Ile
20
Ala Leu Ile Ile Gln Lys Asp Lys Val Tyr Gln Gln Val Gly Ser Val
35
Arg Phe Val Val Val Val Val Val Val Val Val Val Val Val Val Val
50
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Gln
65
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
85
Unk His Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
100
Leu Gly Arg Unk Gln Thr Unk Asp Unk
115
120

(11) SEQUENCE DESCRIPTION: SEQ ID NO:823

(1X) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..121

(V1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES

(2) INFORMATION FOR SEQ ID NO:823:

Val Gly Tyr Ile Pro Unk Gln Lys Ile Val Gly Ile Ser Ala Ile Ala
1
Lys Leu Ile Gln Ile Tyr Ser Lys Arg Leu Gln Ile Gln Gln Arg Leu
20
Thr Thr Gln Ile Ala Gln Thr Phe Asp Gln Ile Ile Gln Pro Arg Gly
35
Val Ile Val Val Val Val Val Val Val Val Val Val Val Val Val Val
50
Gly Ala Lys Ala Lys Cys Asp His
65
70

(11) SEQUENCE DESCRIPTION: SEQ ID NO:822

(A) NAME/KEY: misc_feature
(B) LOCATION 1..72

SUBSTITUTE SHEET (RULE 26)

(v1) ORIGINAL SOURCE: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 99 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:825:

1 Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys
5
10

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:824

(B) LOCATION 1...13

(A) NAME/KEY: misc-feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 13 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:824:

1 Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
5
10 Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
20
25 Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Glu Val Gly Ser Val
35
40 Arg Phe Val Val Val Val Val Val Val Val Val Val Val Val Val Val
50
55 Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65
70 Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Glu
80
85 Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Glu
95
100 Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu
105
110 Leu Gly Arg Unk Glu Thr Unk Asp Unk
115
120

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:823

(B) LOCATION 1...121

(A) NAME/KEY: misc-feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE: Helicobacter pylori

(v1) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 149 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:827:

Val Ile Lys Pro His Ser Val Gly Leu Val Arg Ile Gly Ile Cys Leu
1
Ser Leu Gln Val Gly Tyr Gln Leu Gln Val Arg Thr Arg Ser Gly Leu
20
Ala Leu Asn His Gln Val Met Val Leu Asn Unk Pro Gly Thr Val Asp
35
Asn Asp Tyr Arg Gly Gln Ile Lys Val Ile Leu Ala Asn Leu Ser Asp
50
Lys Asp Phe Lys Val Gln Val
60
70

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:826

(B) LOCATION 1...71

(A) NAME/KEY: misc_feature

(1X) FEATURE:

(A) ORGANISM: Helicobacter pylori

(V1) ORIGINAL SOURCE:

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 71 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:826:

Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser Leu Gly Phe
1
Leu Lys Ala His Gln Val Ser Ala Gln Ile Ala Asp Ile Phe Tyr
20
Lys Leu Asn Ala Lys Gln Pro Lys Met Lys Ile Asn His Thr Lys Gly
35
Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala Arg Gln Asp
50
Leu Gln Val Pro Leu Leu Asn Gln Lys Gln Ile Pro Ala Ser Val Arg
65
Tyr Ser Leu Gly Gly Val Val Asp Thr Ile Lys Ala Arg Leu Gly
80
Gln Trp Arg
85
90
95

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:825

(B) LOCATION 1...99

(A) NAME/KEY: misc_feature

(1X) FEATURE:

SUBSTITUTE SHEET (RULE 26)

Met Gln Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1 5 10 15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20 25 30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35 40 45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50 55 60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65 70 75 80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85 90 95
Gly Tyr Phe Gln Ile Leu Lys Gln Ser Ile Leu Ser Leu Thr Pro Asp

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:827

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...149

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:827:

Met Gln Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1 5 10 15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20 25 30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35 40 45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50 55 60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65 70 75 80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85 90 95
Gly Tyr Phe Gln Ile Leu Lys Gln Ser Ile Leu Ser Leu Thr Pro Asp
100 105 110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
115 120 125
Unk Gly Ala Unk Gly Phe Gly Pro Val Ala Ile Thr Ala Ala Ile
130 135 140
Leu Val Ala Leu Gly 145

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:827

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...149

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

100
110
115
120
125
130
135
140
145
Leu Val Ala Leu Gly
Unk Gly Ala Unk Gly Phe Gly Pro Val Ala Ile Thr Ala Ala Ile
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu

(2) INFORMATION FOR SEQ ID NO:828:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:828

Met Gly Ile Ile Leu Leu Ile Val Ala Val Val Leu Phe Tyr Phe
1 5 10 15
Tyr Asn Thr Leu Lys Gly Tyr Leu Lys Asn Pro Leu Asn Pro Lys Thr
20 25 30
Lys Thr Gly Tyr Asp Leu Lys Asn Asp Pro Tyr Leu Val Gly
35 40 45
Ser Ser Pro Leu Asp Lys Phe Lys Gly Thr Gly Ala Tyr Met
50 55 60
Arg Leu Leu Lys Phe Leu Asp Ile Gly Lys Asn Ala Leu Asp Asn Ala
65 70 75 80
Leu Arg Thr Leu Phe Ile His Gly Leu Gly Pro Leu Asn Ser Gly
85 90 95
Gln Gln Asn Leu Ala Lys Gly Leu Leu Asn Gly Pro Val Asp Lys Lys
100 105 110
Glu Asn Phe Gly Ser Leu Cys Gly Ile Ala Asp His Thr His Gly
115 120 125
Glu Tyr Thr Lys Arg Leu Lys Leu Val Gly Phe Leu Met Leu Ala
130 135 140
Tyr Ala Asp Gly Ile Leu Asp Ser Lys Gly Lys Gly Leu Phe Leu Asp
145 150 155 160
Val Gly Ala Phe Leu Gly Ile Asp Asn Gly Asp Phe Asn Gly Tyr
165 170 175
Asp Asn Phe Gly His Phe Asn Ser Ile Gly Ile Pro Met Ser Leu Gly
180 185 190
Glu Ala Lys Asn Leu Phe Gly Ile Gly Thr His Thr Thr Met Gly Asp
195 200 205
Leu Gly Lys Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met
210 215 220
Asn Asp Asn Lys Arg Tyr Ser Gly Gln Asp Phe Ile Ser Leu Lys Lys
225 230 235 240
Ile Ala Leu Ala Ser Gly Leu Leu Asn Asp Leu Lys Asp Ser
245 250 255

(2) INFORMATION FOR SEQ ID NO:829:

SUBSTITUTE SHEET (RULE 26)

Met Asn Gln Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
1
5
20
25
30
35
40
45
50
55
60
65
70
75
80
Asp Gln Ala Met Val Cys Ala Leu Leu His Asp Val Val Gln Asp

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:830

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...527

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:830:

Met Gln Val Gln His Gly Lys Ile Gln Thr Thr Leu Ser Leu Gly Ala
1
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
Val Val Lys Arg Leu Arg Lys Asn Lys Tyr

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:829

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

85	Thr	Pro	Cys	Glu	Ile	Glu	Thr	Ile	Glu	Arg	Glu	Phe	Gly	Asp	Val	110
90	Ala	Asn	Leu	Val	Asp	Ala	Leu	Thr	Lys	Ile	Thr	Glu	Ile	Arg	Lys	115
95	Glu	Leu	Gly	Val	Ser	Gln	Asp	Pro	Arg	Met	Val	Ser	Ala	Leu		125
	Thr	phe	Arg	Lys	Ile	Leu	Ile	Ser	Ala	Ile	Gln	Asp	Pro	Arg	Ala	130
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	Leu	Asp	135
	Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Gln	Thr	Leu	Ala	140
	Val	Val	Lys	Ile	Ser	Met	Ser	Ser	Ile	Lys	Asn	Gln				145
	Thr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	150
	Leu	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Lys	Asn	Gly	Met	Ser	Ser	Ile	155
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	160
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	165
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	170
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	175
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	180
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	185
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	190
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	195
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	200
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	205
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	210
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	215
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	220
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	225
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	230
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	235
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	240
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	245
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	250
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	255
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	260
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	265
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	270
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	275
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	280
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	285
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	290
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	295
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	300
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	305
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	310
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	315
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	320
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	325
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	330
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	335
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	340
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	345
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	350
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	355
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	360
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	365
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	370
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	375
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	380
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	385
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	390
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	395
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	400
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	405
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	410
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	415
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	420
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	425
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	430
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	435
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	440
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	445
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	450
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	455
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	460
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	465
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	470
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	475
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	480
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	485
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	490
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	495
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	500
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	505
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	510
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	515
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	520
	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	Lys	Asn	Met	Leu	Thr	Leu	Asp	525

(2) INFORMATION FOR SEQ ID NO:831:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(2) INFORMATION FOR SEQ ID NO:833:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...325

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:833

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1 5
Ala Val Lys Thr His Asn Leu Gln Arg Val Gln Ala Ser Gly Val Ala
20 25
Asn Asp Lys Gln Ala Pro Leu Ser Trp Arg Ser Lys Gln Val Arg Asn
35 40 45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
50 55 60
Ala Asn Gln Ser Ile Gln Gln Ala Leu Gln Asn Val Pro Gly Val His
65 70 75
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
80 85 90
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
100 105 110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Gln Ile Gly Thr
115 120 125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
130 135 140
Lys Gly Gly Gln Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145 150 155
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Gln Ser Gln Val
160 165 170
Ser Gln Arg Thr Thr Phe Trp Gly Lys Ser Gln Asn Gly Phe Phe
175 180 185
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
190 195 200
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
210 215 220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225 230 235
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
240 245 250
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
255 260 265
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
270 275 280 285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
290 295 300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305 310 315
Gly Gly Phe His Phe
320 325

(2) INFORMATION FOR SEQ ID NO:833:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (VI) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...325

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:833

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
 1
 Ala Val Lys Thr His Asn Leu Gln Arg Val Gln Ala Ser Gly Val Ala
 20
 Asn Asp Lys Gln Ala Pro Leu Ser Trp Arg Ser Lys Gln Val Arg Asn
 35
 Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
 50
 Ala Asn Gln Ser Ile Gln Ala Leu Gln Asn Val Pro Gly Val His
 65
 Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
 80
 85
 Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
 100
 Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Gln Ile Gly Thr
 115
 Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
 130
 Lys Gly Gly Gln Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
 145
 Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Gln Ser Gln Val
 160
 Ser Gln Arg Thr Thr Phe Trp Gly Lys Ser Gln Asn Gly Gly Phe Phe
 175
 180
 Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
 195
 Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
 210
 Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
 225
 Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
 240
 245
 Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
 260
 Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
 275
 Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
 290
 Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
 305
 Gly Gly Phe His Phe
 325

(2) INFORMATION FOR SEQ ID NO:834:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...252

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 834

Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Gln Lys Gly
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Lys Thr Leu Val Phe Gln Met Lys Leu Ala Lys Ser Pro Met Cys Gln
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245
Val Gly Ser Ala Phe Lys Gly Gln Pro Phe Leu Asp Phe Gln
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
Lys Unk Lys Unk Tyr Ile Unk Unk Lys Unk Unk His Leu Unk Val
Phe Asn Gln Ile Tyr Gln Ile Pro Thr Unk Thr Phe Leu Leu Gln Lys
Unk Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Arg Ser Gln Arg
Arg Leu Arg Ala Cys Ala Phe Gly Gln Ala

(2) INFORMATION FOR SEQ ID NO: 834:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(1X) SEQUENCE DESCRIPTION: SEQ ID NO:834

Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Gln Lys Gly
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Lys Thr Leu Val Phe Gln Met Lys Leu Ala Lys Ser Pro Met Cys Gln
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245
Leu Gln Lys Gln Arg Ala Lys Val Gly Val Ile Lys Ala Trp
Gln Gln Lys Asn Gln Asp Leu Gln Cys Asp Val Leu Val Asp Cys Val
Val Gly Ser Ala Phe Lys Gly Lys Gln Pro Phe Leu Asp Phe Gln
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Unk
Lys Unk Lys Unk Tyr Ile Unk Lys Unk Lys Unk His Leu Unk Val
Phe Asn Gln Ile Tyr Gln Ile Pro Thr Unk Thr Phe Leu Gln Lys
Unk Asp Leu Lys Leu Pro Lys Arg Asp Arg Lys Arg Ser Gln Arg
Arg Leu Arg Ala Cys Ala Phe Gly Gln Ala

(2) INFORMATION FOR SEQ ID NO:835:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(11) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...597

(1X) SEQUENCE DESCRIPTION: SEQ ID NO:835

Met Ser Asn Gln Gln Tyr Thr Phe Gln Thr Gln Ile Asn Gln Leu Leu
1 5 10 15
Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Gln Ile Phe Leu Arg

20	Glu	Leu	Ile	Ser	Asn	Ala	Ser	Asp	Ala	Leu	Asp	Lys	Leu	Asn	Tyr	Leu
35																
50	Met	Leu	Thr	Asp	Glu	Lys	Lys	Gly	Leu	Asn	Thr	Pro	Ser	Ile		
55																
60																
65	Gly	Ile	Gly	Met	Asp	Lys	Ser	Asp	Leu	Ile	Glu	His	Leu	Gly	Thr	Ile
70																
75																
80																
85																
90																
95																
100	Ala	Lys	Ser	Gly	Thr	Lys	Ser	Phe	Leu	Ser	Ala	Leu	Ser	Gly	Asp	Lys
105																
110																
115	Lys	Lys	Asp	Ser	Ala	Leu	Ile	Gly	Gln	Phe	Gly	Val	Gly	Phe	Tyr	Ser
120																
125																
130	Ala	Phe	Met	Val	Ala	Ser	Lys	Ile	Val	Gln	Thr	Lys	Lys	Val	Thr	
135																
140																
145	Ser	His	Gln	Ala	Tyr	Ala	Trp	Val	Ser	Gly	Lys	Gly	Lys	Phe	Glu	
150																
155																
160																
165	Ile	Ser	Glu	Cys	Val	Lys	Glu	Gln	Gly	Thr	Glu	Ile	Thr	Leu	Phe	
170																
175																
180	Leu	Lys	Glu	Glu	Asp	Ser	His	Phe	Ala	Ser	Arg	Trp	Glu	Ile	Asp	Ser
185																
190																
195	Val	Val	Lys	Lys	Tyr	Ser	Glu	His	Ile	Pro	Phe	Pro	Ile	Phe	Leu	Thr
200																
205																
210	Tyr	Thr	Asp	Thr	Lys	Phe	Glu	Gly	Glu	Asp	Asn	Lys	Lys	Glu	Val	
215																
220	Lys	Glu	Glu	Lys	Cys	Asp	Gln	Ile	Asn	Gln	Ala	Ser	Ala	Leu	Trp	Lys
225																
230	Met	Asn	Lys	Ser	Glu	Leu	Lys	Glu	Lys	Asp	Tyr	Lys	Asp	Phe	Tyr	Gln
235																
240																
245	Ser	Phe	Ala	His	Asp	Asn	Ser	Glu	Pro	Leu	Ser	Tyr	Ile	His	Asn	Lys
250																
255																
260	Val	Glu	Gly	Ser	Leu	Glu	Tyr	Thr	Thr	Leu	Phe	Tyr	Ile	Pro	Ser	Lys
265																
270																
275	Ala	Pro	Phe	Asp	Leu	Phe	Arg	Val	Asp	Tyr	Lys	Ser	Gly	Val	Lys	Leu
280																
285																
290																
295	Tyr	Val	Lys	Arg	Val	Phe	Ile	Thr	Asp	Asp	Lys	Glu	Leu	Leu	Pro	
300																
305	Ser	Tyr	Leu	Arg	Phe	Val	Lys	Gly	Val	Ile	Asp	Ser	Glu	Asp	Leu	Pro
310																
315																
320																
325	Leu	Asn	Val	Ser	Arg	Glu	Ile	Leu	Gln	Asn	Lys	Ile	Leu	Ala	Asn	
330																
335																
340																
345																
350																
355	Ile	Arg	Ser	Ala	Ser	Val	Lys	Lys	Ile	Leu	Ser	Glu	Ile	Glu	Arg	Leu
360																
365																
370	Ser	Lys	Asp	Asn	Lys	Asn	Tyr	His	Lys	Phe	Tyr	Glu	Pro	Phe	Gly	Lys
375																
380																
385	Val	Leu	Lys	Glu	Gly	Leu	Tyr	Gly	Asp	Phe	Glu	Asn	Lys	Glu	Lys	Leu
390																
395																
400																
405	Leu	Glu	Leu	Leu	Arg	Phe	Tyr	Ser	Lys	Asp	Lys	Gly	Glu	Trp	Ile	Ser
410																
415																
420	Leu	Lys	Glu	Tyr	Lys	Glu	Asn	Leu	Lys	Glu	Asn	Gln	Lys	Ser	Ile	Tyr
425																
430																
435	Tyr	Leu	Leu	Gly	Glu	Asn	Leu	Asp	Leu	Lys	Ala	Ser	Pro	Leu	Leu	
440																
445																
450	Glu	Lys	Tyr	Ala	Gln	Lys	Gly	Tyr	Asp	Val	Leu	Leu	Ser	Asp	Glu	
455																
460																
465	Ile	Asp	Ala	Phe	Val	Met	Pro	Gly	Val	Asn	Glu	Tyr	Asp	Lys	Thr	Pro
470																
475																
480																
485	Phe	Arg	Asp	Ala	Ser	His	Ser	Glu	Ser	Leu	Lys	Glu	Leu	Gly	Leu	Ala
490																
495																
500	Glu	Ile	His	Asp	Glu	Val	Lys	Asp	Gln	Phe	Lys	Asp	Leu	Ile	Lys	Ala
505																
510																
515	Phe	Glu	Glu	Asn	Leu	Lys	Asp	Glu	Ile	Lys	Gly	Val	Glu	Leu	Ser	Gly
520																
525																
530	His	Leu	Thr	Ser	Ala	Val	Ala	Leu	Ile	Gly	Asp	Glu	Pro	Asn	Ala	Met
535																

696

Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Gln Ser Lys
545 550 555 560
Lys Thr Leu Gln Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu
565 570 575
Lys Cys Gln Asp Lys Gln Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr
580 585 590
Asp Gly Arg Ser Phe 595

(2) INFORMATION FOR SEQ ID NO:836:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...156

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:836

Val Asn Leu Gly Ala Tyr Thr Pro Tyr Leu Val Asp Cys Ala
1 5 10 15
Tyr Lys Leu Leu Lys Lys His Val Gly Ile Gln Asn Tyr Thr Leu Leu
20 25
Asp Thr Ala Cys Gly Asn Lys Gln Phe Leu Lys Leu His His Pro Lys
35 40 45
Lys Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn
50 55 60
Ala Leu Ala Asn Pro Lys Arg Gln Asn Tyr Gly Ile Ser Gln Asp Gln
65 70 75
Pro Leu Ile Ile Val Gly Asn Pro Tyr Asn Asp Arg Thr Ser Phe
85 90 95
Ile Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Gln Ile Asp Asn
100 105
Asp Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala
115 120 125
Ile Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu
130 135 140
Ile Lys Gln Ala Asn Phe Lys Gln Phe Lys Ala Ile 145 150 155

(2) INFORMATION FOR SEQ ID NO:837:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...157

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:837

Met Lys Ser Ile Leu Leu Phe Ile Phe Val Val Cys Gln Leu Gln
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155
Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr
Leu Arg Lys Gln Asp Leu His Ile Lys Thr Gln Asn Asp Leu Ser
Asn Ala Trp Tyr Leu Pro Gln Lys Ala Pro Lys Gln His Ser Trp
Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Asp Tyr Leu Gly Thr
Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr
His Pro Asn Ile Asn Pro Tyr Lys Arg Asn Gln Phe Lys Phe Gln Ile
Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr
Leu Tyr Leu Asp Tyr Thr Gln Thr Asn Trp Phe Gln Ile Tyr Asn Asp
Pro Gln Ser Ala Pro Met Arg Met Ile Lys Phe His Ala

(2) INFORMATION FOR SEQ ID NO:838:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES
(VI) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...191

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:838

Met Gly Leu Met Gly Val Ser Gln Gly Leu Pro Asn Thr Thr Ser Lys
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125
Phe Gly Ile Gln Phe Asp Ser Leu Ala Asp Val Val Ala Phe Gly Val
Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg
Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg
Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe
Ile Gly Ile Pro Ile Pro Ala Ala Val Leu Val Val Leu Cys Val
Leu Leu Asp Asn Lys Tyr His Phe Leu Gln Gly Asn Thr Gln Lys Leu
Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile

Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile
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Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser Ala
Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp

(2) INFORMATION FOR SEQ ID NO:839:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839

Met Ile Gly Val Tyr Pro Asn Tyr Ser Lys Lys Gln Leu Lys Arg Pro
1
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Val Leu Cys Asp Gln Lys Asp Leu Leu Arg

(2) INFORMATION FOR SEQ ID NO:840:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840

Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn His Tyr Cys Arg Lys

SUBSTITUTE SHEET (RULE 26)

Val Leu Thr Ser Gly Asp Met Ile Thr Cys Pro Tyr Cys Gly Arg Ile
 1 5 10 15 20 25 30 35 40 45 50
 Leu Tyr Ala Gln Ser Thr His Gln Ser Asn Ala Gln Pro Pro Lys Gln
 Ser Gln Pro Lys Gln Ser Gln Gln Ser Gln Gln Ser Gln Gln
 Gln Ser Gln Ala Val Arg Leu Ile Val

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:841

(A) NAME/KEY: misc-feature
 (B) LOCATION 1...58

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:841:

1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275
 Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys Lys Gln Gly Ala Lys
 Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Met Ala Ile Ile
 Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val
 Phe Gln Lys Cys Leu Pro Asn Tyr Gln Lys Asn Gln Asn Pro Ser Pro
 Cys Ile Gln Val Lys Pro Asp Ala Gly Tyr Val Leu Lys Asp Ile
 Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly
 Ile Gln Asn Pro Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr
 Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Unk Lys Tyr Gly Lys Pro
 Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Lys Lys Gly Arg
 Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Asp Val
 Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile Asn Ser Arg Trp Ser
 Pro Leu Ser Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val
 Thr Gln Ser Gln Leu Ala Gln Lys Ser Pro Phe Val Met Leu Ala Lys
 Gln Val Pro Asn Ala His Lys Arg Met Gly Asp Tyr Gly Leu Ala Val
 Val Gln Gln Ser Asp Asn Ser Phe Val Leu Ala Thr Gln Phe Asn
 Pro Leu Thr Leu Asn Arg Ala Ser Ala Gln Gln Ile Gln Asp His Gln
 Cys Ala Ile Leu Arg

700

(2) INFORMATION FOR SEQ ID NO:842:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(11) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:842

Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
 1 5 10 15
 Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
 20 25 30
 Ser Ser Ala Val Leu Ser Leu Lys Glu Gly Val Tyr Tyr Ala Ile Gly
 35 40 45
 Phe Leu Leu Phe Trp Val Val Phe Ile Pro Phe Arg Lys Leu Asp
 50 55 60
 Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Ala Leu
 65 70 75 80
 Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Glu Arg Trp Leu Val
 85 90 95
 Ile Pro Phe Thr Ser Ile Thr Leu Glu Pro Ser Glu Pro Val Lys Asn
 100 105 110
 Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
 115 120 125
 Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
 130 135

(2) INFORMATION FOR SEQ ID NO:842:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(11) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:842

Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
 1 5 10 15
 Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu

SUBSTITUTE SHEET (RULE 26)

701

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Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
Phe Leu Leu Phe Trp Val Phe Ile Phe Phe Arg Lys Leu Asp
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Gln Pro Val Lys Asn
Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe

(2) INFORMATION FOR SEQ ID NO: 843:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 843

Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Gln
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Leu Phe Gly Val Lys Gly Asp Gln Ile Leu Lys Gln Ile Val Phe
Arg Asn Tyr Pro Leu Gln Lys Ser Val Leu Lys Gln Pro His Gln Ala
His Met Pro Thr Ile Gln Met Leu Val Ser Asn Pro Pro Tyr Ile Ala
Phe Cys Leu Lys Gln Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp
Asp Ile Ser Pro Lys Ala Leu Gln Val Ala Leu Lys Asn Ile Gln Arg
Ser Val Ser Leu Ala Leu Gln Asn Pro Asn Leu Ser Ile Tyr Ala Ser
Tyr His Leu Lys Gln Ile Gly Ile Gly Ile Gly Ser Gly Cys Val
Pro Gln Thr Gln Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln
Phe Tyr Gly Arg Ser Phe Phe Val Asn Gln His Val Leu Ile Pro Arg
Lys Arg Leu Asn Asp Cys Pro Ile Gln Tyr Leu Leu Gly Ser Cys Asp
Leu Gln Leu Ser His Gln Gln Thr Arg Phe Phe Gln Leu Val Gly
Gly Phe Val Leu Gln Lys Gln Arg Val Phe Leu His Thr His Gln His
Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Gln Ser Gln Ile Leu Leu

702

Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr 225
 Asp Glu Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp 230
 235
 240
 Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly 245
 250
 255
 Val Leu Lys Ser Phe Leu Arg 260
 265
 270
 275

(2) INFORMATION FOR SEQ ID NO:844:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...36

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:844

Met Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu 1
 Thr Phe Gly Tyr Ile Val Phe Lys Unk Trp His Tyr Ser Ala Ile Arg 5
 10
 15
 20
 25
 30
 35
 Leu Ile Val Ile

(2) INFORMATION FOR SEQ ID NO:845:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...129

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:845

Val Ile Glu Ser His Pro Lys Glu Thr Leu Ile Glu Asp Glu Asn Tyr 1
 5
 10
 15
 Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu 20
 25
 30
 35
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 45
 Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser
 Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser

SUBSTITUTE SHEET (RULE 26)

(v1) ORIGINAL SOURCE: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 276 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:847:

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro
1 5 10 15
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Gln Arg
20 25 30
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala
35 40 45
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Gln Ile Ser Lys
50 55 60
Arg Leu Gln Gln Ile Gln Ala Gln Leu Lys Val Ser Lys Gln His Lys
65 70 75 80
Lys Lys Leu Leu Lys Gln Leu Gln Ala Lys Gln Lys Ala Gln Leu
85 90 95
Ile Ile Ser Asp Ala Asn Lys Gln Ala Leu His Asp His Ala Lys Ile
100 105 110
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe
115 120 125

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:846

(B) LOCATION 1...127

(A) NAME/KEY: misc-feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 127 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:846:

703
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr
50 55 60
Lys Met Ser Leu Gln Ser Ala His Lys Asn Gln Leu Gln Asn Ala Phe
65 70 75 80
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Gln Asp Ile Ala Gly Val
85 90 95
Asn Gln Val Lys Gln Leu Leu Gln Val Ile Asp Tyr Leu Lys Lys
100 105 110 115 120 125
Pro

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847

Met Arg Val Leu Gln Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Gln Phe Gln Lys His
Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp
Ile Ala Arg Pro Lys Lys Leu Tyr Asp Gln Lys Ile Thr Pro Phe Lys
Gln Gln Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Gln Asn Leu
Lys Met Asp Ser Leu Gln Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile
Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Gln
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
Ala Gln Ile Gln Phe Gly Phe Gly Ala Leu Ser Lys Asp Lys
Asn Leu Ser Tyr Phe Ile Ile Asp Lys Thr Leu Tyr Asn Pro Ile Gln
Gln Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys
Val Phe Lys Asp

(2) INFORMATION FOR SEQ ID NO:848:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848

Val Ala Leu Leu Gln Pro Ser Val Met Tyr Leu Thr Gln Lys Tyr Gln

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Thr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Asp Tyr
Leu Thr Phe Phe Gly Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met
Gly Trp Val Leu Lys Lys Gly Lys Leu Arg Leu Leu Ser Ala His Phe
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr

(2) INFORMATION FOR SEQ ID NO:849:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849

Val Gly Leu Met Lys Ile Arg Phe Met Gly Arg Ser Val Phe Val Gly
Asp Leu Gly Arg Ile Gly Val Ala Arg Phe Gly Thr Trp Leu
Leu Gly Gly Lys Ala Ile Lys Gly Pro Arg Arg Leu Val Leu Gly
Ile Ala Leu Lys His Gly Leu Asn Lys Leu Leu Lys Arg Val Gly
His Phe Lys Gly Asp Gly Ile Phe Lys Gly Met His Asp Lys
Lys Ile Gly Ser Val Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile
Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe Gly Ala Gly
Ser Gly Gly Val Leu Gly Asn Leu Ala Leu Gly Ser Asp Gly Ile Ala
Phe Tyr Pro Phe Gly Ile Lys Asn Ser Val Val Arg Leu Lys Gly Phe
Tyr Gly Ala Phe Gly Lys Asp Leu Gly Val Leu Gly Pro Lys Arg Ile
Ala Lys Lys Phe Phe Asn Ser Leu Val Gly Ile Thr Ala Leu Ile
Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly Val Phe Cys
Asn Gly Leu Leu Cys Gly Gly Leu Ala Lys Arg Leu Lys Leu Gly
Arg Gly Tyr Phe Phe His Lys His Phe Pro Asn Asp Arg Ser Ile

706

Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys
225
230
235
240

(2) INFORMATION FOR SEQ ID NO: 850:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...151

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 850

Val Ser Asp Ser Asn Ala Leu Lys Gln Val Phe Leu Asn Ile Ser Ala
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Ala Leu Gln Val Asn Ala Ala
Tyr Gln Lys Thr Ala Phe Gln Asn Asp Gln Arg Lys Asp Ser Val Tyr
Phe Asn Val Gln Val Cys Leu Ile Gln Pro Gly Pro Val Lys Ser Asn
His Ala Leu Gln Ala Tyr Ser Asp Ala Leu Arg Leu Gln Leu Lys Pro
Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys
Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile
Ser Val Asn Phe Ala Leu Cys Gln Val Val Gln Lys Leu Pro
Phe Gly Ser Val Gln Asp Thr Pro Ile Gln Gln Val Lys Lys Gln Phe
Lys Gln Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly Val

(2) INFORMATION FOR SEQ ID NO: 851:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:851

Val	Ile	Val	Ala	Trp	Leu	Phe	Arg	Phe	Lys	Ser	Ile	Ala	Phe	Ser	Ile	1
Leu	Ile	Thr	Leu	Val	Ile	Leu	Val	Asp	Ile	Trp	Val	Tyr	Ser	Asp	30	
Val	Arg	Gln	Phe	Leu	Leu	Asp	Thr	Ser	Ser	Phe	Ile	Trp	Leu	Leu	20	
Ile	Ala	Leu	Leu	Ile	Lys	Trp	Gly	Val	Ile	Val	Ile	Ser	Ala	Arg	50	
Cys	Tyr	Gln	Phe	Ser	Gln	Lys	Met	Phe	Ala	Leu	Ile	Gln	Arg	Lys	65	
Gln	Ile	Arg	Gln	Asn	Leu	Lys	Asn	Arg	Ser	Asn	Arg	Lys	Asp	Ala	80	
Asn	Phe	Gln	Lys	Leu	Ser	Asn	Ile	Ala	Gln	Ile	Ile	Ser	Lys	Lys	95	
Gln	Gln	Gln	Ser	His	Lys	Gln	Asp	Ser	Asn	Asp	Gln	Asn	His	Lys	110	
Asp	Lys	Leu	Ser	Asn	Ile	Thr	Gln	Gln	Met	Ile	Leu	Lys	Lys	Gln	125	
Asp	Lys	Leu	Ser	Asn	Ile	Thr	Gln	Gln	Met	Ile	Leu	Lys	Lys	Gln	140	
Gln	Leu	Lys	Ala	Arg	Lys	Asp	Lys	Gly	Asp	150					150	

Val	Leu	Met	Ala	Leu	Unk	Asp	Lys	Arg	Tyr	Gly	Leu	Gln	Ala	Gly	Ile	1
Lys	Tyr	Phe	Thr	Met	Gly	Ala	Met	Ala	Ser	Ala	Phe	Phe	Ala	Met	Gly	5
Ala	Met	Ala	Phe	Tyr	Leu	Leu	Thr	Gly	Ser	Leu	Asn	Leu	Gln	Val	Ile	20
Ala	Met	Ala	Phe	Tyr	Leu	Leu	Thr	Gly	Ser	Leu	Asn	Leu	Gln	Val	Ile	25
Thr	Leu	Tyr	Leu	His	Thr	Gln	Gly	Ile	Thr	Asn	Pro	Met	Leu	Phe	Ala	40
Thr	Leu	Tyr	Leu	His	Thr	Gln	Gly	Ile	Thr	Asn	Pro	Met	Leu	Phe	Ala	45
Met	Gly	Thr	Ile	Phe	Leu	Ile	Gly	Ala	Ile	Gly	Phe	Lys	Val	Ser	Leu	60
Val	Pro	Phe	His	Thr	Trp	Met	Pro	Asp	Val	Tyr	Gln	Gly	Asn	Asn	Pro	75
Val	Phe	Ala	Ser	Tyr	Ile	Ser	Ile	Val	Pro	Lys	Ile	Ala	Gly	Phe	Val	90
Val	Ala	Thr	Arg	Leu	Phe	Gly	Ala	Phe	Ile	Asp	Thr	His	Thr	Ala	Trp	105
Val	Gln	Asp	Ile	Phe	Tyr	Val	Leu	Ile	Leu	Met	Thr	Ile	Thr	Ile	Pro	120
Val	Gln	Asp	Ile	Phe	Tyr	Val	Leu	Ile	Leu	Met	Thr	Ile	Thr	Ile	Pro	125
Asn	Phe	Ile	Ala	Leu	Trp	Gln	Asp	Val	Lys	Arg	Met	Leu	Ala	Tyr	140	
Asn	Phe	Ile	Ala	Leu	Trp	Gln	Asp	Val	Lys	Arg	Met	Leu	Ala	Tyr	155	
																160

Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
 165
 Thr Gln Asp Ser Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
 180
 Phe Thr Tyr Ile Gly Ala Phe Gly Leu Trp Leu Lys Ser Arg
 195
 Gln Lys Thr Trp Asp Gln Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
 210
 Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
 225
 Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
 245
 Phe Leu Ala Val Gln Ser Ala Leu Gln Ser Asn His Ile Leu Leu Ala
 260
 Val Val Met Leu Val Asn Ser Ala Val Ala Phe Tyr Tyr Phe Arg
 275
 Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
 290
 Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
 305
 Ser Leu Leu Pro Trp Arg
 325

(2) INFORMATION FOR SEQ ID NO:852:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...326

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:852

Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Gln Ala Gly Ile
 1
 Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
 20
 Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Gln Val Ile
 35
 Thr Leu Tyr Leu His Thr Gln Gly Ile Thr Asn Pro Met Leu Phe Ala
 50
 Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
 65
 Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Gln Gly Asn Asn Pro
 85
 Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
 100
 Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
 115
 Val Gln Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
 130
 Asn Phe Ile Ala Leu Trp Gln Gln Asp Val Lys Arg Met Leu Ala Tyr
 145
 Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
 160

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325

Thr Gln Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Ala
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
Gln Lys Thr Trp Asp Gln Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
Phe Leu Ala Val Gln Ser Ala Leu Gln Ser Asn His Ile Leu Leu Ala
Val Val Met Leu Val Asn Ser Ala Val Ala Phe Tyr Tyr Phe Arg
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
Ser Leu Leu Pro Trp Arg

(2) INFORMATION FOR SEQ ID NO:853:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1..179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853

Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu Unk Ile Ser Gln Gln
Pro Gln Val Lys Gln Ile Thr Asn Gln Leu Lys Gln Leu Asn
Ala Leu Arg Ser Asn Ala His Phe Ser Gln Val Gln Leu Ser Leu
Lys Cys Ile Val Arg Ile Leu Gln Val Leu Leu Ser Leu Asp Phe
Lys Asn Ala Asn Gln Ile Asp Ser Ser Ser Leu Arg Asn Ser Ile Gln Trp
Lys Thr Asn Ala Gly Gln Ser Leu Lys Leu Lys Met Lys Gln Tyr Gln
Arg Phe Phe Ser Gln Phe Asn Thr Ser Met His Ala Asn Gln Gln
Val Thr Asn Thr Leu Asn Ala Asn Ala Gln Asn Ile Lys Ser Unk Ile
Lys Unk Leu Gln Asn Gln Leu Ile Gln Thr Thr Arg Leu Leu Thr
Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp Asn Ala Asn Asn Gln
Ile Thr Lys Asn Lys Thr Unk Ser Leu Gln Ala Ile Thr Gln Ala Lys
165
150
155
160
165
170
175

Asn Asn Ser

(2) INFORMATION FOR SEQ ID NO:854:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:854

Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240
Lys Ala Tyr Gly Cys Gly Leu Asp Asp Trp Gly Val Met Ile Asp Thr
Asn Ile Lys Gly Leu Leu Thr Arg Leu Ile Leu Pro Ser Met
Ile Glu His Asp Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240
Val Lys Glu Unk Ser Unk Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
Thr Tyr Ala Tyr Pro Gly Gly Unk Val Tyr Gly Ala Ser Lys Ala Unk
Thr Arg Gly Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
Ser Arg Val Arg Gly Lys Asp Lys Pro Lys Ser Gly Tyr
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly

(2) INFORMATION FOR SEQ ID NO:854:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1 Val Phe Ala Thr Asp Ser Ser Phe Ser Met Gly Leu Thr Met Ala
5
10
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855

(A) NAME/KEY: misc-feature
(B) LOCATION 1...160

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:855:

Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe
1
5
10
15
20
25
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35
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45
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215
220
225
230
235
240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

(A) NAME/KEY: misc-feature
(B) LOCATION 1...240

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

711

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 146 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:857:

Met Tyr Gly Val Lys Ile Lys Asp Lys Ile Asp Lys Gln Leu His
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
Asn Asn Asp His Leu Phe Gln Gly Leu Phe Gln Lys Arg Trp
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys
65 70 75 80 85
Lys Ser Met Arg Ile Asn His Phe Leu Gly Leu Phe Pro

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:856

(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(1x) FEATURE:

(A) ORGANISM: Helicobacter pylori

(v1) ORIGINAL SOURCE:

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(A) LENGTH: 94 amino acids

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:856:

Ser Ala Tyr Gln Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln
20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160
Ala Leu Leu Leu Leu Ala Ile Leu Leu Asp Leu Ser Phe His
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu
Gly Arg Phe Val Phe Gln Pro Gln Leu Ala Lys Asn Ile Val Lys Ala
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg
Phe Lys Gln Gln Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1..146

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:857

Met Thr Leu Asp Asp Leu Gly Gly Ser Leu Asp Pro His Cys Phe
1
Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Gln Arg Leu Ser
20
Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Lys Asp Ser Ala
35
Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly Ile
50
Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Gln Leu Phe Gln Lys
65
His Asn Ala Leu Gln Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala Lys
85
Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu Ser
100
Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Gln Lys
115
Ile Ala Ile Leu Arg Gly Gly Gln Thr Leu Ser Trp Asn Leu Gln Gln
130
Ile Ala 135
145

(2) INFORMATION FOR SEQ ID NO:858:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES
(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1..204

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:858

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
20
Gly Ser Gly Gln Lys Ile Pro Asp Leu Asp Val Phe Met Pro Gln Arg
35
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Gln
50
Lys Thr Ala Ser Val Leu Asn Pro Asn Gln Ala Lys Asp Leu Ser Lys
65
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
85
Gln Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
100
105
110

714

Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Gln
 115 120 125
 Ser Ser Leu Gln Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
 130 135 140
 Lys Lys Gln Arg Gln Asn Pro Gln Ile Leu Asn Gly Ser Arg Arg Lys
 145 150 155
 Arg Ile Ala Leu Gly Unk Gly Leu Gln Unk Gln Ile Asn Arg Ile
 160 175
 Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
 180 185 190
 Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
 195 200

(2) INFORMATION FOR SEQ ID NO:858:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...204

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:858

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
 1 5 10 15
 Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
 20 25 30
 Gly Ser Gly Gln Lys Ile Pro Asp Leu Asp Val Phe Met Pro Gln Arg
 35 40 45
 Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Gln
 50 55 60
 Lys Thr Ala Ser Val Leu Asn Pro Asn Gln Ala Lys Asp Leu Ser Lys
 65 70 75
 Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
 80 85 90
 Gln Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
 95 100 105
 Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Gln
 110 115 120
 Ser Ser Leu Gln Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
 125 130 135
 Lys Lys Gln Arg Gln Asn Pro Gln Ile Leu Asn Gly Ser Arg Arg Lys
 140 145 150
 Arg Ile Ala Leu Gly Unk Gly Leu Gln Unk Gln Ile Asn Arg Ile
 155 160 175
 Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
 180 185 190
 Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
 195 200

(2) INFORMATION FOR SEQ ID NO:859:

(1) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

(A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...173

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:859

Met Gly Val Leu Gly Met Phe Ala Phe Ser Trp Val Phe Leu Phe
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Gln Lys Asp
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
Gly Cys Gln Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Gln
Asn Asn Thr Leu Gln Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
Gln His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
Leu Lys Asn Ala Phe Gln Val Leu Thr Asn Ala Gln Ile Pro Leu Gln
Leu Arg Arg Tyr Ala Tyr Arg Asn Arg Pro Lys Arg Gln Gln Lys Arg
145 150 155 160 165 170
Gly Phe Lys Gly Cys Gln Cys Asp Ala Arg Gly Phe Gly

(2) INFORMATION FOR SEQ ID NO:860:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:860

Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly Phe Asp Cys
1 5 10 15 20 25 30
Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Phe Ile Gln Pro Ser

716

Asn Ile His Ala Val Lys Leu Val Gly Gly Ile Pro Lys
 phe Leu Thr Asn Asn Ile phe Thr Lys Val phe Tyr Gly Ile Leu Lys
 Lys His Gly Asn Asp Gly Ser phe Lys phe Leu Leu His Asn Lys Val
 Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile Val Gly Ala
 Val Ala Ser Ala phe Ala phe Leu Gly phe Ala phe Asp Arg Gly Asn
 Ile Leu Asn Thr Ala Leu Ile Tyr Gly Asn His Pro Asp Asn Ile Thr
 Pro Ala Val phe Gly Gly Tyr Asn Ala Ala phe Val Gly Lys Lys
 Val Ile Ser Leu Lys Thr Lys Ile Pro Ser phe Leu Lys Ala Val Met
 Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gly Ser Arg His Leu Cys
 Pro Ser Val Thr Ala Cys Lys Lys Ala Cys Leu Thr phe Arg Met Arg
 Val 180 185 190

(2) INFORMATION FOR SEQ ID NO:861:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..104

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:861

Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
 Gln Leu Ala Tyr Ala Ile Gly Val Ile Gln Pro Val Ser Ile Tyr Val
 Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Gln Leu Lys Cys
 Val Lys Ser Val phe Lys Leu Thr Pro Lys Gly Ile Ile Gln Ser Leu
 Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe
 Gly Arg Gln Leu Gln phe Thr Trp Gln Lys Thr Asn Lys Val Gln
 Gln Ile Lys Ala phe Lys Arg
 100

(2) INFORMATION FOR SEQ ID NO:862:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...355

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:862

Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys Tyr Phe Leu
1 5
Ile Val Leu Ala Leu Gly Phe Val Gly Ile Asp Ser Leu
20 25
Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe
35 40
Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser
50 55
Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile Lys Ser Asn
65 70
Gln Tyr Thr Ala Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu
85 90
Ser Pro Ile Phe Leu Ile Ser Leu Phe Thr Ala Val Tyr Val Gly
100 105
Leu Asn Ala Thr Pro Phe Val Tyr Met Gln Gly Lys Thr Gln Asn Leu
115 120
Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Gln His Leu Leu Val Lys
130 135
Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln
145 150
Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Gln
165 170
Ser Tyr Ala Gln Ala Lys Gln Ala Phe Phe Gln Asp Lys Tyr Trp Ile
180 185
Leu His Asp Thr Thr Ile Tyr Gln Met Pro Leu Ser Phe Gln Leu Gly
195 200
Ala Asn Ala Leu Asn Thr Thr His Leu Gln Thr Phe Lys Thr Leu Lys
210 215
Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala
225 230
Val Ser Ile Thr Asp Ala Leu Ser Leu His Ala Leu Val Arg Gln
240 245
Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile
260 265
Leu Pro Phe Val Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser
275 280
Pro Ser Leu Ala Arg Tyr Gln Asn Leu Ala Leu Gln Lys Phe
290 295
Ile Ile Thr Leu Val Trp Gly Leu Phe Phe Ala Leu Gly Lys
305 310
Phe Ser Ile Ser Gly Ile Leu Ile Pro Gln Ile Gly Val Leu Ser Pro
325 330
Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn
340 345
Lys Arg Leu
355

(2) INFORMATION FOR SEQ ID NO:863:

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

Val Gln Lys Ala His Pro Asp Val Phe Asn Leu Leu Gln Val Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Asp Gln Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Phe Lys
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
Gln Gln Asp Leu Ser Gln Ala Asp Lys Gln Lys Ala Ile Lys Gln Ser
Leu Arg Gln Phe Phe Lys Pro Gln Phe Leu Asn Arg Leu Asp Gln Ile
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile 85 90

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:863

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...92

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:863:

Val Gln Lys Ala His Pro Asp Val Phe Asn Leu Leu Gln Val Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
Asp Gln Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Phe Lys
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
Gln Gln Asp Leu Ser Gln Ala Asp Lys Gln Lys Ala Ile Lys Gln Ser
Leu Arg Gln Phe Phe Lys Pro Gln Phe Leu Asn Arg Leu Asp Gln Ile
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile 85 90

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:863

(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...92

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1 5 10 15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
20 25 30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
35 40 45
Leu Leu Val Leu Asn Lys Gln Ile Lys Asn Ile Gln Lys Gln His Ala
50 55 60
Leu Unk Thr Lys Gln Phe Gln Lys Lys Arg Gln Thr Asn Gln Unk Leu
65 70 75 80

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:864

(A) NAME/KEY: misc_feature
(B) LOCATION 1...82

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:864:

Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1 5 10 15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
20 25 30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
35 40 45
Leu Leu Val Leu Asn Lys Gln Ile Lys Asn Ile Gln Lys Gln His Ala
50 55 60
Leu Unk Thr Lys Gln Phe Gln Lys Lys Arg Gln Thr Asn Gln Unk Leu
65 70 75 80
Ser Unk

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:864

(A) NAME/KEY: misc_feature
(B) LOCATION 1...82

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iii) HYPOTHETICAL: YES

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:864:

Seq Unk

(2) INFORMATION FOR SEQ ID NO:865:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHEICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...233

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:865

Leu Ser Leu Met Unk Val Leu Asn Ala Lys Gln Cys Val Unk Pro Ile
1 5 10 15
Thr Arg Ser Val Lys Tyr His Gln Ser Ala Gln Ile Arg Ala Leu
20 25 30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
35 40 45
Lys Leu Val Lys Asp Lys Pro Ala Val Ile Leu Asp Leu Asp Gln
50 55 60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65 70 75
Ile Lys Tyr Thr Pro Gln Thr Trp Asp Lys Phe Gln Lys Gln Gly Ser
80 85 90
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Gln Tyr Ala Asn Ser
100 105 110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
115 120 125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
130 135 140
Gln Gln Ser Val Leu Leu Lys Gln Lys Gly Lys Pro Lys Ala Val Arg
145 150 155
Arg Gln Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
160 165 170
Thr Leu His Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
175 180 185
Gln Gln Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
190 195 200
Gln Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Gln Asp Gly
205 210 215
Pro Ile Lys Ala Trp Gln Asn Lys Lys
220 225 230

(2) INFORMATION FOR SEQ ID NO:865:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865

Leu Ser Leu Met Val Leu Asn Ala Lys Gln Cys Val Unk Pro Ile
1 5 10 15
Thr Arg Ser Val Lys Tyr His Gln Ser Ala Gln Ile Arg Ala Leu
20 25 30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
35 40 45
Lys Leu Val Lys Asp Lys Pro Ala Val Ile Leu Asp Leu Asp Gln
50 55 60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65 70 75
Ile Lys Tyr Thr Pro Gln Thr Trp Asp Lys Phe Gln Lys Gln Gly Ser
80 85 90
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Gln Tyr Ala Asn Ser
95 100 105
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
110 115 120
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
125 130 135
Gln Gln Ser Val Leu Lys Gln Lys Gly Lys Pro Lys Ala Val Arg
140 145 150
Arg Gln Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
155 160 165
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
170 175 180
Gln Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
185 190 195
Gln Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Gln Asp Gly
200 205 210
Pro Ile Lys Ala Trp Gln Asn Lys Lys
215 220 225 230

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866

Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala
5 10 15

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Gln Asn Tyr Arg Phe His Ser Leu Tyr Leu Phe Gln Gln Asn Leu Asp
 Leu Phe Lys Ile Ser Cys Tyr Phe Ala Arg Tyr Gln Asp Leu Ile Lys
 Lys Gly Ala Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Gln Leu
 Lys Met Asp Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu
 Gln Ile Met Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Gln Asn
 Ile Gln Ser Tyr Tyr Lys Gln Ala Leu Arg Gly Tyr Gly Ser Phe Gln
 Asp Gln Leu Leu Gly Leu Lys Asn Thr Leu Lys Asn Leu Pro Leu Tyr
 Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val
 Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val
 Val Gly Asn Gly Pro Ser Leu Asp Leu Leu Asp Phe Leu Lys Gln
 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235
 Asn Gln Gln Lys Phe Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro
 Leu Lys Ala His Gly Val Lys Val Asp Phe Gln Ile Gln Val Gln Arg
 Ile Asp Tyr Leu Lys Gln Val Leu Gln Arg Ala Pro Leu Gln Asp Thr
 Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala
 Lys Gln Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val

(2) INFORMATION FOR SEQ ID NO:867:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature
 (B) LOCATION: 1...85

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:867

Met Leu Ala Ala Gly Leu Thr Leu Pro Gln Phe Gly Cys Tyr Leu Ser
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
 His Tyr Leu Leu Trp Lys Gln Cys Val Lys Leu Asp Gln Pro Val Val
 Ile Leu Gln Asp Asp Val Thr Leu Gln Ser His Phe Met Gln Ala Leu
 Gln Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
 Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
 Cys Ile Ser Ser Leu

(2) INFORMATION FOR SEQ ID NO:867:

SUBSTITUTE SHEET (RULE 26)

Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly
1
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
Gly Phe Asp Thr Leu Val Pro Asp Ser Phe Ser Tyr Ser Val Phe

(1) SEQUENCE DESCRIPTION: SEQ ID NO: 868

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...289

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 868:

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
Cys Ile Ser Ser Leu

(1) SEQUENCE DESCRIPTION: SEQ ID NO: 867

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...85

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(111) HYPOTHETICAL: YES

(11) MOLECULE TYPE: protein

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala Cys Ile Phe
 Leu Ser Ala Gln Asn Leu Lys Tyr Arg Met Ile Gly Val Leu Leu
 100 110 115 120 125
 Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser Asp Leu Lys
 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205
 Gln Thr Ala Tyr Pro Ile Ala Leu Gln Asn Ser Pro Phe Lys Thr Gln
 Leu Gln Asp Leu Ser Asp Lys Ile Ala Ile Leu Ile Gly Thr Leu Arg
 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285
 Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Lys
 Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Gln Ile
 Met Pro Leu Pro Gln Phe Leu Gln Lys Pro Leu Gln Lys Leu Phe Phe
 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

(2) INFORMATION FOR SEQ ID NO:869:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...436

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:869

Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125
 Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met
 Ala His Phe Gln Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg
 Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro
 Leu Phe Lys Gln Leu Cys Val His Gly Tyr Trp Thr Ile Gln Gly Val
 Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala
 Met Gln Tyr Gly Ile Gln Gln Leu Arg Tyr Phe Leu Leu Arg Gln Val
 Pro Phe Gly Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Gln Arg
 Ile Asn Ala Asn Asn Asp Leu Gly Asn Asp Leu Arg Leu

(XX) SEQUENCE DESCRIPTION: SEQ ID NO:870

Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys	1	5	20
His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu	10	25	30

SUBSTITUTE SHEET (RULE 26)

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Phe Asn Ile Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser
 Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Ala
 35 40 45
 50 55 60
 Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Tyr Leu Leu
 65 70 75 80
 Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala
 85 90 95
 Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp
 100 105 110
 Phe Leu

(2) INFORMATION FOR SEQ ID NO:871:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:871

Met Gly Phe Gln Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
 1 5 10 15
 Ile Val Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala
 20 25 30 35
 Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile
 40 45 50 55
 Gly Ala Cys Gly Val Pro Ser Gln Asn Thr Leu Thr Thr Phe Thr
 60 65 70 75
 Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly
 85 90 95
 Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp
 100 105 110 115
 Phe Ser Val Leu Asp Ser Asp Gln Val Lys Thr Leu Cys Lys Gln Leu
 120 125 130 135
 Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met
 140 145 150 155
 Met Asp Leu Ser Val Gln Asp Ser Gln Cys Tyr Lys Ala Tyr Gln Leu
 160 165 170
 Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Gln Phe

(2) INFORMATION FOR SEQ ID NO:872:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...115

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:872

Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1
Leu His Leu Ser Val Lys Asp Ala Gln Asn Phe Asp Ala Ile Leu Arg
20
Gln Arg Pro Phe Phe Lys Asp Leu Ile Gln Phe Met Val Ser Gly Pro
35
Val Val Val Met Val Leu Gln Gly Lys Asp Ala Val Ala Lys Asn Arg
50
Gln Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65
Arg Ala Asp Phe Ala Gln Ser Ile Asp Ala Asn Ala Val His Gly Ser
85
Asp Ser Leu Gln Asn Ala His Asn Gln Ile Ala Phe Phe Phe Ala Ala
100
Arg Gln Phe
115

(2) INFORMATION FOR SEQ ID NO:872:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...115

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:872

Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1
Leu His Leu Ser Val Lys Asp Ala Gln Asn Phe Asp Ala Ile Leu Arg
20
Gln Arg Pro Phe Phe Lys Asp Leu Ile Gln Phe Met Val Ser Gly Pro
35
Val Val Val Met Val Leu Gln Gly Lys Asp Ala Val Ala Lys Asn Arg
50
Gln Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65
Arg Ala Asp Phe Ala Gln Ser Ile Asp Ala Asn Ala Val His Gly Ser
85
Asp Ser Leu Gln Asn Ala His Asn Gln Ile Ala Phe Phe Phe Ala Ala
100
Arg Gln Phe
115

Arg Glu Phe
115

(2) INFORMATION FOR SEQ ID NO:873:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:873

Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Ser Leu Ser Ile Gly
1 5 10 15
Leu Gly Ile Asn Ile Thr Tyr Ala Val Thr Asp Lys Thr Gln Asn
20 25 30
Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile Ser
35 40 45
Leu Val Unk Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly Ala
50 55 60
Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val Val
65 70 75 80
Phe Gly Gln Met Gly Ala Ile Gly Val Pro Cys Phe Asn Ser Phe Leu
85 90 95
Ala Arg Ala Arg Phe Cys Trp His Phe Tyr Gly Gly Phe Ile Arg
100 105 110
Ala Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
115 120 125

(2) INFORMATION FOR SEQ ID NO:874:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:874

Met Lys Pro Leu His Phe Ser His Leu Asp Arg Gln Ser Gly Asp
1 5 10 15
Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu

20 25 30
 Leu Gly Trp Leu Asn Thr Gln Tyr Phe Leu Trp Pro Ser Met Leu Gln
 40 45 50
 Leu Lys Lys Ile Leu Leu Gln Gln Asn Arg Lys Ser Val Leu Gln
 50 55
 Tyr Ala Gln Arg His Phe Gln Thr Ala Leu Ala Asn Tyr Arg Asn Gln
 60 65
 Lys Gln Thr Ser Gln Ser Leu Leu Lys Ile Phe Asn Asp Gln Gln Ser
 70 75 80
 Arg Arg Ile Leu Gln Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
 85 90 95
 100 105
 Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
 110 115
 Ile Met Ala Arg Ala Ser Gln Leu Gln Lys Thr Tyr Leu Phe Phe Thr
 120 125 130
 135 140
 Leu Ile Asn Lys Tyr Leu 150

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iiii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875

1 5 10 15
 Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Gln Thr Asn
 20 25
 Thr Asp Asp Leu Unk Pro Unk Ser Asp Ala Phe Thr Arg Ser Asp Ile
 30 35
 Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Gln Asn Tyr Gln
 40 45
 Gln Arg Ile Gln Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
 50 55
 Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
 60 65
 Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
 70 75 80
 Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
 85 90 95
 Thr Cys Gln Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
 100 105 110
 115 120
 Leu Lys Gln Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Gln Ile
 125 130
 Thr Leu Asn Asp Lys Val Ser Thr Phe Lys Leu Gln Pro Gln Thr
 135 140
 145 150
 Leu Leu Asp Gln Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
 155 160
 Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Arg Ile Gly
 165 170 175
 180 185
 Ser Val Gln Lys Thr Phe Arg Pro Ser Ser Ala Leu Arg Leu His Phe
 190 195 200 205

(2) INFORMATION FOR SEQ ID NO:876:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...234

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:876

Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp Leu Ile Lys
1 5 10 15
Lys Gln Leu Gln His Asn Ala Tyr Ala Ser Val Ala Ser Gly Val
20 25 30
Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Gln Gly Met Gln Leu
35 40 45
Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Unk Val Gly Leu
50 55
Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val Cys Asp Lys
60 65
Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly Asn Leu Ala
70 75
Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile Gln Asn Tyr
80 85
Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys Ile Asn Arg
90 95
Gln Gln Leu Leu Lys Val Gln Met Gln Ser Tyr His Asp Val Gly Thr
100 105
Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met Met Gln Phe
110 115
Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro Asn Asn Pro
120 125
Leu Arg Lys Val Leu Val Gln Gln Ser Ala Lys Arg Leu Ala Ser Gly
130 135
Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Gln Lys Ser Ile Leu Asn
140 145
Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn His Thr Leu
150 155
His Leu Ile Ala Ile Ala Asp Leu Val Gly
160 165
215 220 225 230

(2) INFORMATION FOR SEQ ID NO:877:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

Leu Met Trp Leu Lys Thr Leu Gln Thr Leu Asn Thr Asp Lys
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80
 Ala Leu Gln Gln Phe Ser Lys Thr Met Gln Ala Phe Lys Thr Lys Leu
 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160
 Ser Asp Thr Leu Arg Gln Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240
 Trp Gly Gln Ile Gln Ile Lys Asn Leu Thr Pro Gly Ser Gln Asn Leu
 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320
 Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
 325 330 335 340 345 350 355 360 365 370 375 380 385 390
 Arg Phe Asn Asn Gln Gly Gly Cys Gly Asn

(2) INFORMATION FOR SEQ ID NO:877:

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES

(V1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...394

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:877

Leu Met Trp Leu Lys Thr Leu Gln Thr Leu Asn Thr Asp Lys
 1 5 10 15
 Ala Leu Gln Gln Phe Ser Lys Thr Met Gln Ala Phe Lys Thr Lys Leu
 20 25 30
 Ile Gln Ser Ala Asn Asp Val His Ser Gln Thr Ser Arg Ala Ala Ile
 35 40 45
 Ala Asn Asp Leu Gln Arg Leu Lys Gln His Met Ile Asn Val Ala Asn
 50 55 60
 Thr Ser Ile Gly Gly Gln Phe Leu Phe Gly Ser Lys Val Asp Arg
 65 70 75
 Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Gln Asp Leu
 80 85 90
 Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
 95 100 105
 Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
 110 115 120
 Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met
 125 130 135
 Asp Ala Leu Gln His Ser Ser Leu Pro Gln Val Phe Ile Lys Pro
 140 145 150
 Ser Asp Thr Leu Arg Gln Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
 155 160 165
 Asn Asp Pro Lys Gln Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
 170 175 180
 Ser Ser Phe Lys Gln Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
 185 190 195
 Gln Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
 200 205 210
 Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
 215 220 225
 Trp Gly Gln Ile Gln Ile Lys Asn Leu Thr Pro Gly Ser Gln Asn Leu
 230 235 240
 Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
 245 250 255
 Leu Arg Ser Ser Gly Lys Arg Val Thr Gln Tyr Val Lys Ser Ala Phe
 260 265 270
 Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
 275 280 285
 Asn Pro Lys Val Leu Gln Ile Pro Ser Val Phe Val Thr Lys Asp Asn
 290 295 300
 Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Gln Ile Phe Gly Asp Lys
 305 310 315
 Val Gln Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Gln Ser Ala
 320 325 330
 Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
 335 340 345
 Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Gln
 350 355 360
 365

733

370 Arg phe Asn Asn glu Gly Cys Gly Asn
385
390

(2) INFORMATION FOR SEQ ID NO:878:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val phe His Lys Lys Ile Ile
1 5 10 15
Leu Asn phe Ile Tyr Ser Leu Met Val Ala phe Leu phe His Leu Ser
20 25
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
30 35 40 45
Leu Val Gly Gln Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly phe
50 55 60
Leu glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65 70 75 80
Gln Asp Lys Gln Leu Ser Ala Gln Ile Gln Ser Asn Val Thr Tyr Tyr
85 90 95
Unk phe Lys Arg Cys Lys
100

(2) INFORMATION FOR SEQ ID NO:878:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val phe His Lys Lys Ile Ile
1 5 10 15
Leu Asn phe Ile Tyr Ser Leu Met Val Ala phe Leu phe His Leu Ser
20 25 30

734

Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
 35 40 45
 Leu Val Gly Gln Arg Leu Val Trp Asp Lys Leu Thr Leu Gly Phe
 50 55 60
 Leu Gln Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
 65 70 75 80
 Gln Asp Lys Gln Leu Ser Ala Gln Ile Gln Ser Asn Val Thr Tyr Tyr
 85 90 95
 Unk Phe Lys Arg Cys Lys 100

(2) INFORMATION FOR SEQ ID NO:879:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1..265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879

Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Gln Lys
 1 5 10 15
 Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn
 20 25 30 35
 Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile
 40 45 50 55
 Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu
 60 65 70 75
 Lys Tyr Ser Leu Gln Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser
 80 85 90 95
 Val Ala Gln Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys
 100 105 110 115
 Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu
 120 125 130 135
 Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val
 140 145 150 155
 Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly
 160 165 170 175
 Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys
 180 185 190 195
 Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr
 200 205 210 215
 Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu
 220 225 230 235
 Ser Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile
 240 245 250 255
 Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Gln Leu
 Ala Asn Gln Arg Gln Arg Gln

735

265

260

(2) INFORMATION FOR SEQ ID NO:880:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xt) SEQUENCE DESCRIPTION: SEQ ID NO:880

Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
1
Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Gln
20
Thr Phe Ser Lys Gln Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
35
Tyr Ile Gly Leu Ser Lys Lys Pro Gln Ser Val Leu Lys Asn Thr
50
Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
65
Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Gln Ile Lys Gly
80
Ala Lys Asp Leu Ala Tyr Lys Ser Gln Thr Phe Ile Leu Arg Leu Gln
95
Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Lys Cys
110
Val Ile Gln Ala Phe Arg Phe Asn Asp Val Ala Lys Asn Asp Ile
125
Leu Gln Lys Lys Lys His Lys Lys Asn Gln Ile Ile Lys Arg Leu
140
Asp Phe Lys Gly Leu Leu Asp Ile Leu Gln Lys Asp Phe Leu Ser Tyr
155
Leu Gln Lys Asp Leu Pro Asn Ile Tyr Gln His Gln Gln Asp Leu
170
Gln His Lys Gln Leu Gln His Lys Lys Asn Gln Ile Ile Lys Arg Leu
185
Asn Ala Gln Lys Gln Arg Leu Lys Gln Lys Leu Gln Lys Leu Gln Asp
195
Pro Lys Thr Leu Gln Leu Gln Ala Lys Gln Leu Gln Thr Gln Ala Ser
210
Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Gln Asn Arg Val
225
Ile Leu Lys Asp Phe Gln Asp Lys Gln Cys Met Ile Gln Ile Asp Lys
240
Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
255
Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Gln Gln Asn Leu
270
Lys Gln Lys Ile Ala Phe Lys Gln Asn Gln Ile Asn Tyr Val Arg Asp
285
Ala Ala Gln Ser Val Leu Gln Met Phe Met Pro Val Lys Asn Ser
300
Lys Ile Lys Arg Pro Met Asn Gly Tyr Gln Val Leu Tyr Tyr Lys Asp
315
Lys Ile Lys Arg Pro Met Asn Gly Tyr Gln Val Leu Tyr Tyr Lys Asp
330
335

736

Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
 340 345 350
 Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk
 355 360

(2) INFORMATION FOR SEQ ID NO:880:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 1...363

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:880

Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
 1 5 10 15
 Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Gln
 20 25 30
 Thr Phe Ser Lys Gln Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
 35 40 45
 Tyr Ile Gly Leu Ser Lys Lys Pro Gln Ser Val Leu Lys Asn Thr
 50 55 60
 Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
 65 70 75
 Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Gln Ile Lys Gly
 80 85 90 95
 Ala Lys Asp Leu Ala Tyr Lys Ser Gln Thr Phe Ile Leu Arg Leu Gln
 100 105 110
 Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Lys Cys
 115 120 125
 Val Ile Gln Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
 130 135 140
 Leu Gly Ala Leu Pro Pro Asn Ile Tyr Gln His Gln Gln Asp Leu
 145 150 155
 Asp Phe Lys Gly Leu Leu Asp Ile Leu Gln Lys Asp Phe Leu Ser Tyr
 160 175
 Gln His Lys Gln Leu Gln His Lys Lys Asn Gln Ile Ile Lys Arg Leu
 180 185 190
 Asn Ala Gln Lys Gln Arg Leu Lys Gln Lys Leu Gln Lys Leu Gln Asp
 195 200 205
 Pro Lys Thr Leu Gln Leu Gln Ala Lys Gln Leu Gln Thr Gln Ala Ser
 210 215 220
 Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Gln Asn Arg Val
 225 230 235
 Ile Leu Lys Asp Phe Gln Asp Lys Gln Cys Met Ile Gln Ile Asp Lys
 240 245 250
 Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
 255 260 265
 Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Gln Gln Asn Leu
 270 275 280 285
 Lys Gln Lys Ile Ala Phe Lys Gln Asn Gln Ile Asn Tyr Val Arg Asp
 290 295 300
 Ala Ala Gln Gln Ser Val Leu Gln Met Phe Met Pro Val Lys Asn Ser

737

305 310 315 320
 Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
 325 330 335
 340 345 350
 Lys Thr Glu Unk Arg Met Ile Unk Gly Cys Unk
 355 360

(2) INFORMATION FOR SEQ ID NO:995:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(16) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...822

(11) SEQUENCE DESCRIPTION: SEQ ID NO:995

60 120 180 240 300 360 420 480 540 600 660 720 780 822
 GACGACGTA GTTCTTTT AAGATTGTA GCTATGCGAT TATGTTTGAT CTTAATTAA
 AGTAGAGAG TAGCGATGG ATACGCAAG CAATTAGCTT TAAAGATTG TTTGGTAGG
 TTATGTTTAT TTACGACCCCT TGGTAGCGAA CACCTTGAGC AAAAAGGGA TTATATTAT
 AAGGAGAGG AGCCTTATA TATAGCGAA TATGAGCGAG CGCTTCTT TTATAAGAGC
 GCTATTAAA ATGGTAGTC GCTTGCTTAT ATTCTTTAG GGCATCATGTA TGAATAAGT
 AGGGTGTA CTAAGAATTA CAAGAAGCG GTTGAATATTT TCCAAAAGC TGTGATTAAC
 GATATACCTA GAGCGTATA CAATTGGGC GTGATGATA AAGAGGCTAA GGGAGTTCT
 AAGATGAAA AGAAAAGCGGT GGAATATTTT AGAATAGCTA CAGAGAAAAG TTATACTAAC
 GCTATATCA ACTTAGGCAT CATGTATATG GAGGCGAGGG GAGTTCCAAG TAACTATGCG
 AAAGCAGAC AATGTTTATG AAAGCGATG CATAGGCGCA ATGTGGAAGC TTATATCTC
 CTAGGGATA TTATTTATAG CCGGAATGAT CAATTGGGTA TTGAGCCCGA CAAAGATTAAG
 GCTGTGTCT ATATAAAT GCGCGCCGAT GTAGTCTCTT CTAGAGCTTA TGAAGGGTTG
 TCAGGCCCT ACCGGTATCG GTTAGGGCTG GAAAAGATA AAAAAAGCC TGAAGAAATAC
 ATGCAAAAAG CATGCCATT TGACATTGAT AAAAATTGTA AG

(2) INFORMATION FOR SEQ ID NO:996:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(16) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996

```
ACGATGAAAA ATACATCCGTC ATCAACGACT TTAACAATGA ATGACACCAT TCCCGCTATC
GCTACCCCTT TAGCGAAGGG ACCGATTAGC ATCATTAATA TCAAGCCGCCA TAACGCCCTA
AACATCCCTC AACACTAC CCAAAAAACA GACTTCACCC CCAAGTATAGC TTACGCTGTC
GACATTTTCT CTGATGGCGT TTATTGAGC AAAGCGCTAG TGAATTATTT CAAGCCCCC
TAATAGTTTC CCGGTGAGAA TGTGTGCGAA ATCCATGCC ATGGAAGCCC CTTTATAGC
CAAAATATCC TTCAAGCTTG CTGGAATTTA GGGGTAGGC TCGCTAAGC GGGGGAATTT
AGCAAAAAAG CCTTTTAA CCATAAATG GATTGAGCG AGATTGAAGC GAGCGTTAC
CTCATCCCTT GTGAAGATGA AAGCGTT
```

(2) INFORMATION FOR SEQ ID NO:997:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997

```
ATCTAATTT ATCGAGCTC ACAAGAGAC GACCGCCTT GCGTGTGCG TTGAAATAA
GAGCGATGA TTGAATACTT GAATCCAT ATCAAGCTCA TTGATGAGAT GATTGCAAGC
GCTATGAG ACAGAGAGAC TTGAATAA GCGAGAGATG CGATGCCAAGC TTGGGTGAT
AAGCGGTAT TTGAAGACC AGATAGTAC GCGCAATACG CCGCTGTAT TGAATTGAT
GTGCGAGAAA TCACGGAGCC TATTTGCGA TCGCTTATG ACCCTTATG CGTGCTACT
TTGAGCGAAG TTGAAGCGG TAAGACCGG AAAAGACCCC AGGCTATTT TGAAGTGTT
ATTGCTCTT GCATGACGA TATTGGCAT TTCAAGCCT TTGGTGAAT CGTTAATAAC
GCCCCCTCCA GTCAAGCACG CTTTGGGTA GTCCACCCCA GTAAATATGA CGAACAGAAG
GAGGCTTATG AGGCTTATTT TCGGATTTT GGGGTGCCC GGGCAAGAC TGAAGTACCA
GGCTGTAGCT TGTGCATGGG CAATCAAGCG AGGTTAGCG ATAAATGCGT CGTTTCTTCT
ACTTCCACAC GGAATTTTGA TAATCGTATG GTAGAGGGG CTAAAGTGT TTTGGGCACT
GCGGAGCTTG GCGCGGCGCTG CGCTTACTA GGAAGATCC CCACTAAGA AGAATACATG
AATTAGTGA GTGAAAAAGT AGAGAGCCAA AAAGACAAGA TCTATCCCTA CATGAACCTT
AACTTAATGG AGAATTTAG GCTC
```

(2) INFORMATION FOR SEQ ID NO:998:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (11) MOLECULE TYPE: DNA (genomic)
 (111) HYPOTHETICAL: NO
 (1v) ANTI-SENSE: NO
 (v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1290
 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:998

AAAATGCCAT ACCCTTAAG AAAAAAGATT TTCAAAAGCC TTTAATTGTT TTTTAAAT
 GTTGTATGA TAAATTTGCA TGCCAAAGCC TATCTGTGTT CTCTTTGCCC CCCAGCGCAC
 CAGAAATGCA TTGAGAGACTG TTGAGAGTGT TTGAGAGTGT TGAAGAGACTG GATGCTGCAA
 CAGAAATGCA TTGAGAGACTG TTGAGAGTGT TTGAGAGTGT TGAAGAGACTG GATGCTGCAA
 AATCAATCT TTCTTTTGT ATCCCAATAC GATGATGATG ATCCCAATAC GATGCTGCAA
 ACTTATGCA AGGCAATCT AAACAATAC AACCCTGAT TCATCGCTTC TCAAACTCCA
 GCTAAGAAA GCTATGAGCC TAAGATTGAA TTAGCGATT TACTGCTTAA AAGGTGTG
 GCGCGTTATG CGATTTTATG GATGATGATG GATGATGATG GATGATGATG GATGATGATG
 GATGATGATG TCAAGAGCTT TGACAGCGAT GAAGAAAGCC CTGAAATTT AGAAGAAACC
 TATAAGAAA TTGAAAGAAA AAAATTTCCCT TTATGATGCG CTTTATTTGAC TAAAGAGGCG
 GTGAAATTT TGCTCCAAA TAAGACTATC AATACCCCTA CTTATGTTCC TACGGTGAAT
 AAAAGCGAAT TAGAAAATCA TACCAGAGCT TCTTAAAGC AGCGCTTGT TTTTGGGGGG
 ATTGATATTA AAGAGCAATT AGGCAATGCT GCACTTTCA TTAGCCCTTA TTGCGCCCGTG
 ATTGATGAGG CCTGATAGGT GAAAGGCTTGA GGCAGCTTCA GGAATTTCA GAGTCTTTA
 AAGCTGAGG TCAAAACACA AGAACAAT TCTTACAAAC AAGCGACCAG TTTTCTTAA
 AATTTAGAA AACTGATGC GTTTTAAAT AATTTAAAT TAAATTTGAA CACCCCTTAC
 ACTAAAAGCG GTCTGATCT TCTCAATA GGGCTTTAG AGTTAAGCC TCTTAAATC
 CTTCCACAC AAATCAATTT CAACCCCTCT TACTCTTGC TCACCCAGCC TAAAGACAGG
 AAAAATTTAT TCAATGTCAT TCCCTTGCA AACAGCGATG AAACCTGAT AGAATACGCT
 TCTTATTTAG AGAGCGAATT AAGCGATGAT TCGGTGAATT ATCCAGCGCG GATAGGCGCT
 GAGATGTTT TAAACACGCT AGATCCGCAAT TTAAAGAT CTTTCAAGA GATTTGAA
 GACATTCAC CAATCAAAAT TATCAGGCTT TAGGTATTC TTTTGAGCCC 1290
 1260
 1200
 1140
 1080
 1020
 960
 900
 840
 780
 720
 660
 600
 540
 480
 420
 360
 300
 240
 180
 120
 60

TATTACATA ATTAATTGAA TACTTTTAT TTAAATGGT TTTAAGAAA GATAGACTAT
 TATCGAGTGC GAAATTTAA AAGGATTTGT GCGGTGTTAA AATTCACAAA ATTACCCCTA
 TTGTTGTTTT CCAATCTTTA TAATCAAAAGC CCTTATTTGG CTTTGAATTA TAAGTTTAGT
 GGGTAGCCCG AATCTGTTTT TAAAGTGGGG TTAAACCAAT CCAACTCAA TTCCAAGAAA
 GGGATTTTCC CTACAGCCAC CTTTGTAAAC GCCACGATCA AGCTTCAAGT GGATTTCCAAAT
 300
 240
 180
 120
 60

740

CTGCTCCCTA AAAACATTGA AAAACACACG TTAATAATAG GCGTTGGGGG GATTTTGAAG
 GCGTCCCTT ACATTTCCAT CAACACGCTC ATAGACGCTA AATCTATAGCG
 TCAGAACTTT TTAACCTCAT AGGCGCTGG TGGGGGTTTT TAGGCAACGC TCCTTGAAAA
 GACTCCCTCA TAGAATCTGA CGCTCACACG CGTAATTAATG TGTGTATATA TTCTTATATG
 TTTTATCTT ATGCGGATTA ATTCCACCTA AATTAAGGC GTTATCTCTC TAACATGAT
 TTTATAGTT CCTACACACA GGGTTTTGAA CTGATATAA AAATCAATTG TAAATATAGC
 TTAATAGTT TTAGCTCTTT TGGAGAGGCG TTAGCTTTTG GCGAATGAT ACCGATTTG
 TATGCCCTA TGTAACTGA AGATGGCAGA AAGAAAGTTT ATGATGGCAT CCATGCCCGC
 CAACCTATTT TTCTTAGCAA GCATGTTCAA GTCATGCCCTT TTGCTTATTT TTGCCCCAAG
 ATTACGGAG CGCCCCGGGT TAAATATCAT ATTGATAGCA ACCCGAAATTT CAAGAAGCTTA
 GGGTAAAGG CTCAAAACAC TATTAATGTG ATTTCCCTG TTTATGCTAA AGATTTATAC
 GATGTGATTT GCGTTAATC TAAGATTTGC GATCGGCTTTT GATCCACCAA
 CGCTTGAAT ACAACGAAT TAACTTTGCG TTTGCTTAT ACCAAATTT TGGCAACGCT
 AACGCAAGA TTGCTTGTGA TGGTAACCC ATCCCTTTTA ATTATAGAAA TAAACAGCGTT
 TATGTGGCG TCTTCACTAA CGCTATTAAC GCAGACGCCG TTTCTTGGTA TGTCTTGTG
 TATGGGGGTG ATAGAGGGGT TTTATGGGT ATTTAGGCA GATACACTTA TGCCACTAGA
 GCGAGCGAAA GATCCATCA CTTGAACTTG GGTATTAAT GGGGTCTCTT TGTAGAGTT
 CATGTGAAT TAGAATACTA TGTGCTCAGC ATGCACAAAG GCTATGATTT AGACTATCTC
 ACCGGCCCTT TCAACAAAGC CTTTAAAGCT GACGCACAAG ATAGAGATTA CCTTATGTT
 AGCATGAAT TCTTTTTT

(2) INFORMATION FOR SEQ ID NO:1000:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(111) ANTI-SENSE: NO

(11) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...762

(11) SEQUENCE DESCRIPTION: SEQ ID NO:1000

GTTACCGCG GGTGGCTAT CGCTATAGC ATGCTCATG ACTCATCTGT GGTAGTGTG
 GAACACGCTT TGAACAAATT GAGCGCTAAC ACTAACAACG CTAAACTCCA TCAATCTAT
 CGTCAATGCA AAGAAATCGC CGTTTCACTG GTGACCGGGG TGTGATCAT TATGTCTTT
 TTGTGCCCCG TCTTAACCTT ACAGGGGTTA GAGGCGAAGA TGTTTAGGCC TTTAGCGCA
 AGCATGTGTG ATGCGCTTTT AGGCACCTTA GTCTATCCA TCACTATCAT TCTGTAGTG
 AGCTCTCTTG TCTTAAAGC CACGCCCCAT AGCGAAACCT TTTTAAAGAG GTTTTAAAC
 AGAATCTACG CCCCTTATT GGAATTTT TGTCAATAAC CTAAAAAAGT GATTTTGAAG
 GCGTTGTTTT TTTTATCGC AAGCCCTTCT TATTTCCCTT TGTGGGGAA GAATTTCTATG
 CCTGCTTTAG ATGAGGGCGA TGTGGTTTTG AGCGTGGAAA CCACCCCCTC TATTTCCCTA
 GATCAATCTA AAGATCTCAT GTTAAACATT GAAAGCGCGA TTAACAAACA TGTCAAGAA
 GTTAAAGCA TTGTCGCGCG CACAGGGAGC GATGAAITTG GGTGGAITTT AGGGGGTTTTG
 AATCAACCG ATACTTTAT TCTTTTCTC CTTAATAAGC TTAATAAGAC TT

(2) INFORMATION FOR SEQ ID NO:1001:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

741

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...471
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1001

60
120
180
240
300
360
420
471
TGGTGTTC TAACATGCTA TGGTAGTGTG ATAAAGAAAG CCTATATAG AGGAGATCTT
ATCGGTATAG TTGAATAATT ATTCTTGTG TCGTTTGTG CGTATATAGTAG TCGGTTCCGA
GCGGATTTAG AAACCGGAGC CAAAAAGAGCG GTAAAAAAATT TTACAAACTC
CAATAAAACC ATGGCTCAGT AAACGAGACT AAAAAAGATA AAGAGCTTTA TGATTTCAC
AAAAATAGCG GATTAGAACG CGTGGATTTA GAAAAAGAGC CTAAACCTTA AGGCCATAAA
AAAAAGCGAT AAAAAATTTA TAACAACACT GCTAAAAACA ATATCGCTGA AGGGGTAGC
ATGCCGATG TGAATTTCA TAAAGCCCTA TCTTTTGGCG CTATTTTGA AAGGACTTAA
AGCAAAAAA CCAATACAT GACGCGCGGG TTGATGATG ACATCCGTTT T

(2) INFORMATION FOR SEQ ID NO:1002:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...675
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1002

60
120
180
240
300
360
420
480
540
600
660
675
CCGAAAAATG CACCGCTTGC CATGCCATTG AATCCCAAAA CATTCCAGCC CCTATGAGTA
GCCCTAGTGC GAGCAACTCT TTGGGGGTGC GGCACACCGA ATTTAAGCCA TGTGCGGGGG
GTTTGAACG CGAGTTCTT AGCCCACTTC ATCAAAAGACC CGGTGAATAAC GCGCAATAATG
AGCCATAAGT TCAACGATGA AAGGCCCTAT CCTATGCGCG CGTTTCTCA ATTTAGCGAT
CAAGATTGA GCGATTTGT GCGGTATCTC ACTTCTATTT TGCCTAAAAA TTGAGCGGAT
AAGGAAGTCT TCGCGCAAGG TTGTCAAAGG TGCCATAGCC TGATTTATAG TAAAGATTAAG
GCCTTAGCG ATCCTAAGA TTAGCCCAAT TATTTAGGCT TCATGCGCC TGATTGTCC
ATGATGATTA GGGCTAAGGG CGAACATGCG TTGAATGTTT TCATCAACGA TCCGCAAAAAG
CTTTGCCCTG GCACACCCAT GCCTAGAGTG GGAATTGAATG AAAAAAGCTCA AAAACCAAGTC
ATTCTTATT TTGAATAAGC GGGCGATAGG AAAAAAGCATG AAAGGAATAC TTTAGGATTT
TGGAGCGAAG TGCAT

SUBSTITUTE SHEET (RULE 26)

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...852

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1004:

ACTTGGCGGT ATCAACTAGC CTGATTAA GCCTAATCC AATGATTAA AAGCTAGAG
ATTGAAATTT ACAGAAATTT TGAGCACCCTT AAGATGAGAA AAGCCGCTT ATAGGGGTAT GAGGTTAGA
GAAAGCGGAG TTTTAAAG CAATAGCCTTG TTGAGCCTTG AAAAAGAAAG CGCTTCCTGGC
TTTGGCCACC CCACACATTA GGAATTTTA TTAAGCCCA TCAACACGAT ATCCGATAT
AAATGCAAG AGTTTAA AGCTGCTTT AGTTAGCTC AAAAATTA CAATCAAAAT
ATGACCAATC GTGTCAGTA TCTTTTAT GATGAAATAG AAAGCGGCTT GCACCATACA
AGCTTTTA ATTTGCTT TGGGGTTT ATCAAAATCT TTAATTAAGT GAGCATCTT
AGAAAGTCTG TCTATATCCA AATCAAGAT GAAGAACAAC CGCTAGAGAA AAGTCCCAA
AAGAAATCTG ACATGCTT ACATGCTT AACCTAATA TTTAATATC TAAATCAATA
GAATATCTA TTGTAATTC TCTTAAAGCA TTGAAATTT TACAAATTT AAGCAAGAA
CATTTAATTT TAGATTAAT CGCTCAAC TATAAAGAA ATGCGATCTT TATTCCTATA
CCATCCCTTT CCCCAGTAC AATGACTTAT GAATTTGAAA GCCTAATCT AGGTTAATC
CATATGACAA ACCTTATTA CACACACATA ACGAAGCCAC AGCTCCCAAT TTCTTCAAT
ATCAATACC CCACACACAG CAGTTACAGC AAGACATCA ATTTGAAATG CGATGATGCT
AACAACCGCT ATCCCATAG TATCCGACT GAATTTGAA AGCTTACTAT CCCTTTACT
AGTAATTTCA GAAAAATCA ACTGATGCC GACAACTTAA AAACCTTTT TTATCAAGA
TTTACCGGCT ATCCCTAGC CAATCAAGT AGCTTCTC CTGAACATGC CGTGAATATT
TTTACCGGCT AAACGAGT GGTAAACG AATCTTTAG AAGCTCTTA TACCAACACA
ATTGAAATTT ACAGAAATTT TGAGCACCCTT AAGATGAGAA ATTTAATCT CATCACTTT
AAGCTAGAG

(1x) SEQUENCE DESCRIPTION: SEQ ID NO:1003

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1143

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1003:

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 291 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1006:

GATTAAGAAA TACTTTTAT TATTCAAGA AATTATAG AATTCAATCA AGTTATGAC
CCATAGAGCC ATATTGGCT GAGCGCTTA GTCCACTTT CGCTATTGC GCTCTTTT
AATCTCTTA TGTCTTTA ACTTAAGG TATAAGCGCT GGTTTTAA GCTTAGCGCT
TCAATCCCTTA TTCCGTATT TGTATATAA ATGCTGTTC AATGCTGAG CGCGAGTTT
TTCTTAGGCT TTCTTTAGC CTGTCGCCG ATCCGATGA TTGATATCG TCGCATTTT
CTTCAACCC TTTCAGTGA GTCCGGGTAT TTGATAATCT TAAAGAAAG CGTTCAATCC
ATCACTTAG ATCAACCGCAT TTATGTAAT TTGATGGCT TTGTTTGGC TCATTTT

(1x1) SEQUENCE DESCRIPTION: SEQ ID NO:1005

(B) LOCATION 1...417

(A) NAME/KEY: misc_feature

(1x) FEATURE:

(A) ORGANISM: Helicobacter pylori

(1v1) ORIGINAL SOURCE:

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 417 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1005:

ACCAATGTT TATTCCTTG TGTAGATC AAATTTGT TAATCCTTA AGAGGCAT
GATTAAACC ATGCTTAT CCAATTAGCA AATATCACCA TTAAGACGA CTTATCCCC
AGTAAAGG CCGTGTGA AGACGTTTG ATCAATCTA GCAATGTGG CATGATAAA
ATCAATAAA GCCTCAACC AGAGGATTC TATAAGCGCT TTTAAGGCTA TCGATTTCT
CAATAAACCG GATTTGATTT ATCTTAGAA GCCACAGAA AGATCCCTCC TTGTCCTC
TTCAAGCGTG AAGTGTAA GGGAGCGTC TCTTAGGCT ATGCGTTGAA TCGCACTTT
TTGCACCTTT TAAGGGCTTA TCGGTGTGTT TCTAATGAAG GCAATTGAC TACCCCTAT
TTAGTCCAAC GAGAACCCG CCGTAATGCG GATATTACA TCCCTAGCC CAAGCCACCC
TTTCAAGTCA TTAGCCCCCA AAGCGCTAGA AAATGAAG AAACCTTAAT TAAAGTGTG
CGTTATGGCA CAGGCAAAA CGCTCAATTT GAAAGGCTAT ACATAGAGGG CAAGACAGGC
ACGGCTAGGG TTGCTAATAA CGGAAGCTAT AGCGGAGT CCTATAACAG CTCTTTTTT
GGGTTCGCTG AAGATGAAG GCAAGTTT ACTATCGCG TGGTTATCTT AGGCTCGCAT
GGCAAGAG AGTATACG TAGCAAGATT GCAGCCCCCA TTTTAAAG AATCACCGAA
ATTATAGTG GTTACATTA CCTATCGCC TCTATTGCCA TTCAAAAGC TTGGAATAA

(1x1) SEQUENCE DESCRIPTION: SEQ ID NO:1004

(v1) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...291

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1006

```

CCTAAGCTA AAGCGTTG CCTAATAAT CTAATGAGTA AAGAAGCAT CCGTTCCCT
AACAGCTT TTTCATACC TAAACCCAA ATAAAGCGA CAAACACAGT CCACACCGTT
TTATTCAT ACCGCTCAA ACCCAGCAA ATGGCTTAT TACCGCTCGT TACCCTCATG
CTCGTCCAA TTTTAAAGC TATACACAGC ACTAAGCGGC TCAACCGCTAT CAACACCTGAT
GGACCGGCT CTAAATTA CCCTATATC ATGCCATGA AATACAAA A
291

```

(2) INFORMATION FOR SEQ ID NO:1007:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1596

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1007

```

AGAACGAT TTAAGGTGT TAGAAAATG GCATTAAGG TATTATTATT CTTTGTCTT
TTGTTTGC AAGCAGAGA TAAAGGCCA GAATTATCAT CTATACAAA ACAAAATGCT
TTGTTGATA AAAAATCTCG GTGCTGAAA TTGGTGAGC CTTTGTGAAA
TTGTTGATA TGCCTGAAA TAAAGGGGAT AAAATCTCGG TTGGTGATCA AACCAATTG
TAAACAGCTCA ATAAATGCG CGACCCGGTAT TCTTAAAGG GTTGAAGCGT CAAGCCCTCGA
TCTAATAATG CCGTCAATAT CCGTACGGGA TTGCTTAAAG AATACACGGG TATTACCTAT
AAAAAGGTTT GCGATGCGCGT GATTTTTCG GTTACATTTG ATTCTGATTT TAAAAAAGCG
TTTGTGCTTA ACATTTACAT TTTCACACCA ATTTACAGCCA TTTTGGGATG TTTTGGGATG
ATTTAGAGA ACCTAACCCT TACCACTTAC AGCAATTAAC AGAAGAGCGGG CCGAATTATC
GCTAAGGGGA CGATATTTT TATTGCGCAT GTGTGATA TTCTATATGT GCACATTACG
CTCGGTGCT TTATCATTTT CATTTGGGGG AGCGTGATG TTGGCGATAG GGTTCGTATC
CTCGGTGCT TTGCGAAGCG GCGCTTAGCG ATTGCGATG AGGATTTATT CATGAGCTG
GTTTGAAGG ATTAATCTT TCTTTTCT TATTGATAA ACCTTACTTA CTGGTAAAG
TACATTGAAA ATATGAGCG CGTCTTATAC GTGAATTAAG CCAATTAACTT CGTGAATG
TTTATGCGG CCTTTTGA GCGTGTGTTT GCGTGTGATT TAAAAATCAT TTCCAGTAAA
GAAGCTATA GCATTTGTA ATCTCAAGTT AAAAACCAAGC TTTTAAATTT GCTTTATGTG
TTCAGAGGG CTCAAAAAT TCTAAAAAC AGATCCGGA TTTCACAAA AGACACAGCAT
TTGATATAA GCGCAATAT AAGCGATGAG ATTTATCAAA CTCAGAGCCA AGCGTTAGAA
TTAGAGAGT TTTAAGGCT TTATGATCAA AAACACCAAGC TTTTAAATCA GTGGCACCGT
ATTCTTTCA TCAAGAGCAT GCGTTTAAAG CATGAAAATC TTTAAAAATA CCAAGACTCT
GAGCGCCCA ATATCCCCAA TATCCCTTAT ATGCTTAAAC CATTTGCGAT CATTTGATGC
TTAGAGTCCC AGCAAAAAAT GTTGAAGC TATGCGTCA ATCTTTTA GGACTTGATA
AAAAATTAAC AACCAAGGA TTTATTAAG ATTAGCACT TAGAGCATAC CTTAAGAGCT
AAAAATTTA TACTGAAA TACGAAAG GAGAGCGTGA GCGAGCAATT AAGGCGCGTTA
TTGTTGATA AAAAATCTCG CAAAGACGAT AACGTGTGTT TGAATAAATTT TGAATAAATTT
TTGTTTGC AAGCAGAGA TAAAGGCCA GAATTATCAT CTATACAAA ACAAAATGCT
120
AGAACGAT TTAAGGTGT TAGAAAATG GCATTAAGG TATTATTATT CTTTGTCTT
1500

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GAGAAATAAATG TCCATATGCG TTAATGACGAC AGCAAGCTGC TTAAGTGA TGCTGATGCT 1560
CTAGGCGATG GTTTGGGAA TAAAGGGA CAAAA 1596

(2) INFORMATION FOR SEQ ID NO:1008:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...1041

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1008

CGAGTGAAG GAATGCAAGA AATCTTAATC CCTTAAAG AAAAAGCTA TAAAGTGT 60
TTGGGGGAC TGCTGAAAT AAAATTGAA CAAAGGCGG TCATCAATTAG CGATTAGCATC 120
TTGGGGGAC TGCTGAAAT AAAATTGAA CAAAGGCGG TCATCAATTAG CGATTAGCATC 180
TGCGTGATAG AGTCCGGGGA AAAATACAAA AATTTTCAT CATTAGAGCG GATTTAAAC 240
AACCGCTTGA AATGCCAATT AACCGCGCAT TCTTTAATGA TAGCCCTTGG TGGGGGAGTG 300
ATAAGCGATA TGCTGGGGGT TGCGAGGAGT AATTATTCA GGGGGAATTGA TTTTATTAT 360
ATCCCTACGA CTTTACTGCG TCAAGTGGAT GCGAGCGTGG GGGGGAAGAC AGGATCAAC 420
ACCGCTTAG GCAAGAACCT AATCGGATCG TTCCACCCAGC CTAAAGCCGT TTAATGAT 480
TTAGCTTTT TAAAGCCCT TGAAGAAAG GAAATTCAG CCGGGGTTC TGAATCAT 540
AAAATGCGCG TGCTTTTGA TAAAGACTTG GTAGAAAGAT TAGAACAAG GATTTTAA 600
GATTGTTAG AAGAGTAAAT CTTCAAGC GTCAATATCA AAGCTCAAGT CGTTGTTCAA 660
GATGAAAGAG AGCGAACAT CAGGCGCTGG GTGAACATATG GGCATACCTT TGGCATGCTG 720
ATGAAAGAG AGACCAATTA CAGCGGATTT TGCATGCGC AAGGATCGC TATGCGCATG 780
CGCATGCTA ATGATTTAGC CCTTTCTTGA GGCATGCTCA CTTTAAAGAG ATACGAACGC 840
ATAGAAATTT TATGAAAGAA ATTGATCTG ATATTCAATT ACCAAATCAC TGAATTTCAA 900
AAATTTAGC AACGTTGTT TTAGACAAA AAAAGCGAG ACCAAACCCCT AAAATTTCATT 960
TTGCCTAAG GTGTCGAGC GTTGAAGATT GCCTCTCAT TCCCTAAGAG AACGATTTTA 1020
AAGTGTTAG AAAATGCGA T

(2) INFORMATION FOR SEQ ID NO:1009:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1..588

(*) SEQUENCE DESCRIPTION: SEQ ID NO:1009

```
AAATCAAGA GTATGAATT AAGAGAGAGG AAAATCATG CGTTTCTAA ATTTTAGAA
AACCTCACCG CTCCTTTTAA ACCGATCAAA AACCGCTCGC TTGTTTGGC GTTAAGGTTT
TGATTCCTTA CTTTTCCTT GTTGCTTTT TTAATCTTAA GCGATGTTT TAGGCTCATTA
TCCAGTAAAG ATTTTCTTAA TGTGATCCAG TCTCACCCCTA AACAACTCT AATTGAAGAT
GAAATTAAT TTATGCTTAA CAAGGCTCTT TATTAACCA ACAAGAAGC CTTTTAAGG
GTTTATAAA TCCAGAGAG CATGCCCAT GAAAAACAG AAAGTTAAG CAAGCTTCT
GTTATCAATC TAGCGTTGCT TTTTTCAT TCTAGCATG TTTTGGGAT CTTTGGCGT
TTGCCCAAC GATTGACAC TAAATGAGT TTAGAAGAGC CGACAAAAA CGAATTAGAA
AATGCATTCC AAGATACGA TCGCTAGGG GTCCGTTTG AAGACATTG AGGGGTGAAT
AAGTCAAG AAGATTAAT AAGATGATA GATTATTAA AAAAAACC
```

(2) INFORMATION FOR SEQ ID NO:1010:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..537

(*) SEQUENCE DESCRIPTION: SEQ ID NO:1010

```
ATGAAACCAT TGCATTTT ACACCTGAC AGAGAGCAAT CAGCGCATG GGGTTTATC
ATTAACAC TTATTTT AGGGTTTT TCTTATG GTTGTTGA TACCGAGTAT
TTCTATGCT CTAGCATGCT GAATTTAAA AAAATCTCTT TAGAAGAAA TCGTAAAAAA
AGCGTTTAA AATGAGCGCA AAGGCATTTT GAACAGACCC TAGCAACTA CCGCAATCA
AAGCAACCA CGCAATCTT GTTAAGAT TTATATGATG AAGGTCAG GCGGATTTA
GAAAAAGAT TTAATAATG TTTGACGCC TATTAATCA AACCTTGT CTCTCAAAAC
CCCTCCCAAA AAACCAAT TTATATCATG GCTAGAGCGA GCGAATTGA AAAAACTTAT
CTTTTTTCA CCTAATCA CAAGTATTA CCGAGCGCTC AAAGCCATT GCCCTTAAG
```

(2) INFORMATION FOR SEQ ID NO:1011:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1356

[illegible]

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(14) ANTI-SENSE: NO

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...333

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1012

333	CBAAGCCAAAC	TAAAAAGAGT	CTCTAAATGCC	TAT
300	TGTAAATTT	TAAATCCCAT	AATGATTTT	AAAAATCGTTT
240	TATCAACAGC	GTTATAGAGC	GTTGCTCTA	ACCGTCTTTT
180	TATAAACAT	CTGTCTTTT	AAAGCTTTT	TTAGGTTTG
120	GCAAGCGAT	TAAAGTCG	ATCTTGCAAT	CAGATTTTGG
60	AATCATCAGC	GAAATACGAG	CCGCAACAA	TTAGAAAGC
			CGTTGATCC	CTTAGAAGAGA
			AAAGCCCTAT	ATTAAGGCTT
			AATTCATGCT	GTTTCTCAA
			GTTATAGAGC	CTGTGTAAGT
			TAAATCCCAT	AATGATTTT
			TAAAAAGAGT	CTCTAAATGCC

(2) INFORMATION FOR SEQ ID NO:1013:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...600

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1013

AAGCCATGA AAGAATCTT TTACATAGAG GAATGACTT GCAGGCGGTG TTCTAGCGGG
ATTGAAGCT CTTAGAGC TAAAGTTT GTGAATTT TAGAAGTGA CTTTAAAT
AAGAGCGCTA ACATGAAT TAGAAGAT GAACCAAT TAGACGAAT TTTTAACTC
ATTGAATAAC TGGTTATAG CCTAATAAA ACTTAGCAG AAGAAAAAA AGAATTTT
AGCCATATG TTAATTAGC GTTGGCGGT ATTTCAGCG GTTTTGTTGT GTATCTTCT
AATGGGCGCGA TGCTTAGCCC TAGCCTTTTA CCTGAAGACT TGCTTAGCAT TAACCATCAT
AGTAATTTT TAAAGCGTTG CTTACAGCTT ATAGGCGCGG TCATTGTCAI GCATTGGGG
AGGAATTTT ACATTCAAGC GTTAAAGCC TTATGGCACA GACAACCCAA CATGAGCAGC
CTATCGCCA TAGGCACAG TGCTGCTTA ATTACAGCCT GTGGCAATG TATTGGTTT
ATACCAATCA TTATACCAT CAGTGTCTT ATGGCAATTA TTATTTGAA AGCGTGTGCG

AAAGAGTCT TATGCTTAT TACCCCTCT TATCTTTCC CCAATCTTT TACCCCTAGC
AGTATTTT TTAGCAAT TACGCTTCA GTTACCAAT TGTCAATGCG
TGTTGGTTAG TGTTGGCGAG TCTTATTTA GATGCGCTG ATGGCGGTG GCAGAAGCTT
ACCAACCA CTAGCAAGTT TGTTATGAA TTGACTCTT TAGCTGATGT GGTGCGCTTT
GAGTGGCCC CAGCCTTAT TACTTACTT TATGTGGGT ATACTTTG GCGTATAGCG
ATGGCGGTGA GCGCTTGT TGATTTT TGAGCGATAC GATTAGCGCG ATTCAATATC
AGCACCAACA CAAAGCATC CTATCTTCT ATCGTATCC CCAATCTCTG GCGGCGGTG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1014

(B) LOCATION 1...723

(A) NAME/KEY: misc_feature

(1x) FEATURE:

(1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 723 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1014:

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(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1782 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (11) MOLECULE TYPE: DNA (genomic)
 (111) HYPOTHETICAL: NO
 (14) ANTI-SENSE: NO
 (15) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (16) FEATURE:
 (A) NAME/KEY: misc_feature

(2) INFORMATION FOR SEQ ID NO:1016:

753
 720
 660
 600
 540
 480
 420
 360
 300
 240
 180
 120
 60

TTAGAGATTG GAGATATTAA AGAATTTCG ATT
 AAAAGATTAG AATCCAAA AATTCGTTAA AATTCCTTGT GGGCGGTGTA TCAAGCTTTC
 GCTTATTG GTTGCAATG GCTTTAGAA GAATATTTTA AAAGCGTGCT AGTCATGGAT
 TTGAAGCGT TCAACCGAT CAAAACAAGC ACTTTTGAAG GTTGAGTAG CAAAATAGAG
 CCTAACGAT CAGCGCGGT TTCTACGAGT CTTTCAAG AATTACAGA GATGCCCTT
 AAAAAGAGT TGCTTTAG CGCTTCAAA CGATTAGCTA ATATCAATTA AGACAGAAAC
 AAAATCATTC AAAAGTCAA AGCTTTAAA CGCTTTTAG ACAATCCTTA GAGCGCTCAA
 ATGAGTTGA ACCCTCTAT TATAAGAGAT GTGTTAACA CCAACGAGCG AGACATGTGT
 TATCAAGCT TTGATTAGA GGTTTTGAAG AAGTTTAC TGAAGCGCTT TCATTAATTTA
 TACGGGTTAG AATTGATT GAAGCGGAT TTAATAAAC TCTTGAAG AGTGGCGGTT
 TCTAAGATC CTTGCGGT AGCGCGTT AGTTTGGC TATGAAAT CATCGCGCAT
 TTAGCTGA AATAGACAG CCTGTTTCT CTTTTTACG TGGTAAAT CCTAGCGGA
 TATTGCCC CAGCGAAA CCCCCCTT CCCTCTAGT TTTTAGTTC AATCGTGCT

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1015

(16) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...753
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (11) MOLECULE TYPE: DNA (genomic)
 (111) HYPOTHETICAL: NO
 (14) ANTI-SENSE: NO
 (15) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

723
 720
 660
 600
 540
 480

GCA
 TAGGCATCA TTGCGTGAT CTTTTHAAG GTAAATAAT CTTTTHAAT AAAATAAAGC
 TCGTAGTGT TTGCGCGCC TTAGAGCT TTAGAGCT TTAGAGCT GTATTTGATC
 CCTAATTTA AAAAGTCAA GTGAATCT AAGCTTTCA TCTTAGTGT GATCTTTTA
 AAGTTATTT TAGCTTAT TGTCTTAT GGGTGTCTA TGTGAGCAA TATCCGCTAC
 TTGCTGCTC TTGCTGCT AATGATAT AATACCAT TCTTGAAG CAATACCGAA

[illegible]

```
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
```

(ix) FEATURE:
(A) NAME/KEY: misc.feature
(B) LOCATION 1...603

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1017

360	CTTAGAAGAT	TGATCGCTA	GAAGTCTCAT	TCATCGAAGC
300	AGATCAACCG	TTATCTTTA	TGAAAAAGAT	CGCTCAAAAT
240	TTGCCCTGAA	GATCATCTCT	TATCTGGCG	CTGGTTGAC
180	CGCAATAGCC	AGATTTGAA	AAATTAACCT	AGAGGCTTTA
120	AAATCGCTTT	TGAAAAATT	GAAGGCGCT	CGCTTTCCA
60	GAATACCTGAA	CATTCTTAA	AAAGAAAGTC	AAAGGCGCTT

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603
 600
 540
 480
 420
 360
 300
 240
 180
 120
 60
 0

(2) INFORMATION FOR SEQ ID NO:1018:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: m1sc_feature

(B) LOCATION 1..1620

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1018

1620	TTTAGTGAAG	GGAGCTTTGA	GCTTTTAGG	CAAAAAACA	ACCCCTATG	AAGATGTTCT
1560	TTAGTGAATG	GAATCCCTTAC	AGAGAGATCCC	TTAATCCAAAC	TTAGATTTATG	AGAGTTATG
1500	GCTCTTTTA	AAACCTTTAT	CGCAAAAGAA	AGAGGTTCTA	TTGCTTTTGA	AAAGATCTC
1440	AAACAGGCTT	TCACTTATTT	AAATGAAGTG	GAATGCGATCG	CTTCCCTTGC	CCCCAAAAGC
1380	GTGAAGAATA	GGGATCTTAT	TGTTGTCAAA	CTCAGCAAAAT	TAGGGAGCCT	CCATTTAGAT
1320	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
1260	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
1200	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
1140	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
1080	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
1020	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
960	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
900	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
840	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
780	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
720	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
660	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
600	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
540	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
480	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
420	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
360	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
300	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
240	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
180	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
120	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA
60	GAATCTCTATG	AGATTTGTCA	ACGATTTGCG	TACTATGGTCC	TTTTCACAAA	CGCCTTTAA

(2) INFORMATION FOR SEQ ID NO:1019:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1365 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(*) SEQUENCE DESCRIPTION: SEQ ID NO:1020

(B) LOCATION 1...201
(A) NAME/KEY: misc_feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1020:

60 CAGTCAAGAT TACTCAAAA CCAAAAGTTT TACTCAAAA CAGTCAAGAT
120 TCGAAGATCC ATTTCATCCG TATAGGGGGG ATTCGCATTT CAGGCTTAGC CAAATACCTT
180 AAAGCCGCAAG GGGCTTAAGAT CAGCGGATCT GATATGCCCC TAAGCCCCCTAG CGTTAAGTAT
240 TTGAAGCTT TAGCGCTTAGA AATTAATATC CGCATGATC CAAAGCGGAT CAACCATCA
300 GATGTCATCA TCCATTACAG CATTAATCAA CAGACATAA CCGAATACA AAGGGCTAAG
360 GAATAGAAA TCCCTAATTT GTCTCGTAA GACGCTTTGT ATCTATATCTT TAAAGACAG
420 CGCGTTTGA GCGTGTGTCG GCGTCATGA AAGAGCACTA TCACGCGGCTT GTTACGCGCG
480 ATTGCCCCG GATTATGAGG GCGCATCTCA AAGAGTTGA TTCCAATGTG AAGGCTTTA
540 CGAGAGAGCG CGCATATGAG TTGCGTTT GAAGCCGATG AAGCGGATC AAGTTTGA
600 TTTTCAAGC CTTTTCGCG GATTGTGCT AACACGAGC CAGAACATTT GGAAGCATTT
660 GACCATGAT TAGAACGCTT TTCTTCGCT TATTAATATT TTTAAGACA TCCTCAAAA
720 AAGATGATCT ATAAAGAGA TCCTTTTGA AAAAATATT CTAAGAGAGC CATTTGTTA
780 GAAAAAAG ACAATTTATA TATCCCAATC ATTTTAAAG GTGTGGGGGT TAGCGGAGCC TTACACATTCG
840 TTGAATTGA AAAATTTGG GCGTTTGG GCGTTTGG GCGTTTGG TAGCGGAGCC TTAACGCGCAGC
900 AATCGAGTT TCGCATTTT AAGCGGCTTT GATGAATTA AATTAAGAGA AATTAAGAT
960 AATTATTTGA AATTAAAGG CATTAATAA GCGTTGATA TTTCGCAAA AAAAGCATCTC
1020 ATTTCATTTG ATGATTAAGC CCACCACTT ACTGAATTT GCAACCATTT AAAAAGCGCT
1080 AAGATTTATG CCAATTTAT GAATACGCAA GAATTAATTA TAGTGATCTG GCAAGCGGAC
1140 AAATACCTCT GCTTAATGA CAATTAAGA GAATTAATA AATGTTTTT AGAGCATTTG
1200 GACAGCTTGA TCAATTTACC CGTTTATAC GCGAGTGAAG TTAAGAAGA CATTGATTTG
1260 AAAGCCCATT TTAAGCATTA TAACCCACG TTTATAGACA GGTGCGCTAA AAAAGGGGAT
1320 TTTTGAAGAG TGTAGTCAA TGATAATGTG GTAGAACA GTGAAAAAGC CTTTGTGATA
1365 GCGTTTGAG CGGGGATAT TACCTATCAG TTGAGAGCGG AAATG

(*) SEQUENCE DESCRIPTION: SEQ ID NO:1019

(B) LOCATION 1...1365
(A) NAME/KEY: misc_feature

(1x) FEATURE:

(v1) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

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60 TCGATGCTTTC TACGTAAAT GGTGTAGG TTTTGATCC TTTAAGCC TTTGCGCT

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1022

(A) NAME/KEY: misc-feature
(B) LOCATION 1...516

(ix) FEATURE:

(A) ORGANISM: Helicobacter pylori

(vi) ORIGINAL SOURCE:

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1022:

558 AGCTATCT ATGAACG
540 TTAGAAGC AGCAAGTC ATGCCGGGAA CCCCCTAAC AATCTCATTT TAATGCAAG
480 CCGCATTTA GGTGAGAC AGAGGGCA GCTCAAGTTT GGAATAATCA GGCACAATA
420 AACCTTATG AATGCAAG AGCAACCATT AATGCGGAAA ACAGACCCCT AAGCGGTAA
360 GTGCGTCGCA TCGATATTTT AGCTTTTACT AACGATCAAG GCTTAAGGAA AATCGCGCGT
300 ATGCGCATG AGAATAATG CGTGAATTTCT CTAGCCCTTTA GTAACGGGCT GTAGAGCCG
240 CAAGACTCTA AACTTTAA AACGAGTCAA GACGCGCAAG CTAGGGCCAT TTTAGAGAG
180 AATAACTCA CTATCTTTT GATAGAGAG GAAACATAGA TTCTAACCA ATTGTTCTAC
120 GGCTTGAT CAGCCAGCA CAATAATGAA TCCGCCCCCA TGACTTTGGA TTTAAGGCG
60 AAGCTACATC GTGATCCCA AAAACAAC CCTATCAATG ATCTACTTG GAAATTGTC

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1021

(A) NAME/KEY: misc-feature
(B) LOCATION 1...558

(ix) FEATURE:

(A) ORGANISM: Helicobacter pylori

(vi) ORIGINAL SOURCE:

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1021:

201 GAAGCCATTA GCTTGAAAA A
180 ATGCAAGAG GCTATTTCTAT GAACGCTAGA GCCTTGGCG CGGGCGATGA CATGATCAAA
120 CACAAATAT TTAGAACGAG CAACGTGAAT GCCGGGAGC CCCTAACCA TCTCATTTA
60 GCGTAACCC CCATTTAGG GTGGAGCAG GAAGGCAAG TCAAGTTTG GAAATCAAG

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ACTGGATTGC ATATTTCACA AACACATT ATAGAGCGTT CTTAAATTT CTTCTGCTTTT
 GTGGGGAATT TGTGTGTAATTT TTGGCTTAA AGATTGCGTT CATTTTTGA TTCCAAAAGC
 CTTGAAATCT CCAACCGCTT AGAAGAGATT CAAGCCCAAC TTAAAGTGAG TAAAGAACAT
 AAGAAAAC TCTTAAAGA ATTAGAGCA GCCAAGAAA AAGCTGAATT GATTATTTCT
 GATCGCAAT AAGAGCCTA CACGATCACG CAAAATACG AATTCAAC CAAATGAT
 GTGGAATTT TGATCAAAA TTCTAAGCGG TTGATGATT TAGAAGTTAA AAGATCAAA
 AGAAGATTG TTGAAGCGT TTTAAGAT CTAAAGAGG GTAAAAAGT GTCTTTTCAAT
 GCGCAAGATT GCGTGAATAT TTGAAACAA AGCGTT

(2) INFORMATION FOR SEQ ID NO:1023:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1023

ATGCAAAA GATATTCACA ATAACTCTG TTGTTGGTTT TCCTCTTTT AAAGAATGCT
 GTGGTTAG ACGATAAAA AGCAGCTCTT AAAAGCGTTC AAAATACCCC TAAAAATTTA
 CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAT
 ATGGAAAA GCACGCGCAGTA TGAGTTCCCT AAATTTAAG AATCCCTAGA ACAAAAGCAA
 GAGGAATGCG TAGGAGTCCG CCATGAAGAA TGTGTGCGGT TAGTCATGTT AATAAGCCCT
 AAGCTTCTA TTGAAAACAG CCGGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAACAA
 AGAATCCATG ATTTATATGA GAGGCGCAAA AAGTGAAGA AAAAAATCAAG
 AAAGCCCATG AGCATGAAT GGGCCCTCAC AAATCCCAAC CCTTAAAAA GGAACCCGCT
 AAAAGCGAGA ATAAAAAGCG CTTAACAAA CCTAGCTTGA AAGACGCAAA GATCCCTAAA
 GGGTATTA CT TGCATAATG GGGCTTTTTA AATTCCGCCA GTAAGGATTT TTGCAAAAGC
 CTCAAAAC TT TCCCTCACCA AATGAGAGAA AAGAGCTCCC TCACGCATTA TTGATTGCGC
 CCTTAAAA CCAAGAGAGA AGCCCTAAA CAGCTTGAAA ATCGCGCTAA AAGCTTTAAA
 AATAAGCCCTG CGTTGGTAGA GAAG

(2) INFORMATION FOR SEQ ID NO:1024:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 681 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(2) INFORMATION FOR SEQ ID NO:1026:

ATGAGCCCTT CACAAGCCCT AATTAAGCC AATAAGAGAT TATCGCCCAA AGGCTTTAGG
GGGGGGCTAG AGCTGGAAT TTTATTAAGG TTGTCTCTTG AAAAAGAGAG GGTTTTTC
CACAAGCCATG AGCATTTGGA ATTAAGCCAC GAAGAAGAAA CAGCCTTTT TGAATTTGTA
GGAAGAGCGTT TGAATGACTG CCCCATAGAG TATTTATTAAG GAAGCTGTGA TTTTATGCGG
CGCTCTTTT TCGTGAATGA GCATCTTTTA ATCCACAGCGC CTGAAAACCGA GATTTAGTC
CAAAAAGCCG TTAATATTAT TTCTCAATAC CATTTAAGAG AATTAAGCGA AATCGCATTA
GGAGAGCGGAT GCGTGTCCGT GAGTTGCGT TTAAGAAAAC CTAACTCTC TATTTATGCG
ACGATATT CACCAAAAGC TTGAAGAGTG GCGTTAATAA ATATTGACG CTTTGTCTA
AAGAGAGCGTG TTTTAAAC ACAAAGCCGC CTTTGGGATC ATATGCCAAC GATAGAAATG
CTGTCTCTA ACCCGCCCTA TATCGCTAGA AATTATCCCT TGGAAAAATC CGTCTCAAA
GAACCGCCAG AAGCCCTTT TGGGGGGGT AAGCGCGATG AATCTTAA AGAATTCGTT
TTTTAGCCG CTAAATTA AATCCCTTT TTGCTTTGTA AAATGCGGTA TGACCAAGTTA
AAGAGCTTGA AAGATTTGC GGTATGATG CAGAGTTTA CAGGATTTG

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1025

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...828

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1025:

AGTGGATCT ATTGGAAT CAACTCTGAT GTGTATGTC TTATCATTCG CTGCGCCGAT
CAAAAATAG GCGTATCGT GATTAATTG ATCGGTCAAG AAGAAGTGT CATCAAGTCT
TTAGGTTATT ATCTTAAAA CACTAGAGGC ATTGCTGCGC CTACGGTGA GGGCGATGGG
AATATCACTC TCAATTGAGA TGTGGGGGCG ATGATGGAAA TGGCAAGAG CATTAAGTC
AATATCACTA CCTGATGAA CAGTCAGAA AACACGAAA GCAAAAATTC TCCTAGCGAT
TATGTTGCT TGGCGATTGA TGACAGCAGC ACGGACAGAG CGATTATCCG CAATATGTTA
AAACCATAG GCATCAGCT CTGAAGGCG ACTAACGCT TGAAGGCGTT AGAAATGCTC
AAAAATGCG ATAAATGCT TGAAGATCC TTAGTGAAT TGAAGATCC TAAATGAT
GGCTTACTG TCGCCTCTGA AGTCCGTAA TACAATTAAT TCAAAACCT GCGTATGATC
GCGGTACCA GTGCGTAAC TAAAACGAG AGAATGCGG TCAAAACCT GCGTATGATC
GAATACATCA CCAACCTTA TAGCGGTGA TATTAACCA CCGTAGTGA GCGCAAGCAT
AAATTAGAG GAGACCAATC

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1024

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...564

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1026

60 AAGCGCGTGT GTTCAACCC ACTACCAACA AAAAGGTCCG TCATGCCCA TTCTTTAAA
 120 AACCGTTT TAATCGTTA TACCTTTCT ACCTTGCTT TAGTGGGGT TTGTGTAAGC
 180 TTGTTTTCT TTATGCGAA AATAAACCTT TTGGAACAAC CCATAATACG CATGCAATAC
 240 ACCGTGATG TAGAAGAACG ATTCAAAACG ACCCCCTTTG TTGTGTTGA CGCAGACAAC
 300 TTAAAATCT TAGAAGAACG ATTCAAAAAC ACCCCCTTTG TTGTGTTGA CGCAGACAAC
 360 AGAGTCAAGT TTCTAATAT CGGGTGTGTT GTGGCCCTCT TTAAAATGA CGCTTAATC
 420 AAGACCCCTT ATTTGCGCT TAATAAACAG GCTTTTACC TCACAGACAG CGCCCAACT
 480 AACCGCTTAG GGGTTCTAA AATCATTATT GCAGAAGAGG AATTCAAA AATCTTATC
 540 CCGCTTAATG AATGATAGG CTATGTGTTT TTGGGCGCGG GTTGTGTTGT CGCGCTAATA
 564 GCGATGTGGC TTATATAAT CCGA

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1224

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1027

60 AATATGCTTG ATATATGAT AGATATGATA ATCTGATATT TTATTTGCT CTTTTTACG
 120 ACTCTTACA TTGTAGGCGA TATTTGCAA TTGAATTTA TCCGTCAAA ACTCTGCGAG
 180 AAGCTGTGTT TACTCCACCA AAAGGATTTA GAAAGAACCGG GAATTTATGC TATTAGGAAA
 240 ATGCAATTAT TCAAAATTTA TCAAGGGTGA TCTTTGCTG TTGGGTCTTT
 300 TTGCGTTGA CGCATTTAG AGATCTCAG CATTAATTA ACCTTCTGA AACGCTAGT
 360 TACTGGGTGT TTGCTTGTT GTTTTACCG ATTCAAAACG TTTTAGCTTT ACCCATTAAG
 420 TACTACTA CCATGCATTT GATTAAGGAA TTGCGCTTT CTAAAGGTGAG TTATCGGTG
 480 TTTTAAAGG ATTTTTCAG AGGATTTATG CTCACTTTAG CGGTGGGGTT GTTGTGATT
 540 TACTCTCA TAATGATCAT TGAACATGTG GAGCATTGGG AGATCAAGCT GTTTTGTGTC
 600 GTTGTGTTT TCAATGATTT GGCTAATCTT TTAAACCTTA AAATCGCCCA GCTTTTCAAC
 660 CAATTCACCC CCTTGAATTA TAGGATTTA GAAAGTCAAA TTGAGAGCAT GATGATTAAG
 720 GTGGGTTTA AATCTCAAG CATCTTTGTG ATGACCGCTA TGGACCGTTG CACTTGTATC
 780 AAGCGGTATT TTGAGGCTT GGCTAAAAC AAGCGGTG TGTTGTTGA CACTTGTATC

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(1) SEQUENCE DESCRIPTION: SEQ ID NO:1029

(B) LOCATION 1...897

(A) NAME/KEY: misc_feature

(1X) FEATURE:

(A) ORGANISM: Helicobacter pylori

(V1) ORIGINAL SOURCE:

(1V) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 897 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1029:

ATGAGAAG GACCAATCGT GAGCAATCAA TTAAAGATT TATTGAAG ACAAAAAGAA
GCTAATGCA GCTCTAACA AGAAGACAAT GAAGAATT TGCATTTCAAT TGGCTTATT
ATTGGCGATC AAGATATCGC CATTCCTCAT TTGAATATT TAGAGATCGT CAATCCCAT
GGCTACACGC GAGTCCCTGA AACCCCAAC TATGCTCTG GCGTGTTCAT TTAAAGGGGC
AATGCTCTCC CTTGATCAG TTGCGTTA AAGTTGGCT TGAAGCCGA AAAACAAAAC
AAAGACACTC GTTATTGGT GGTACGCCAT AACGATCGAT CGCTGGGTT TTCAATCGCT
TCTGGACTGA TCCCATCCGA ATCAGCATCC ACTATTGACC CGTCGCAGAA ACTGTGCGCG

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1028

(B) LOCATION 1...432

(A) NAME/KEY: misc_feature

(1X) FEATURE:

(A) ORGANISM: Helicobacter pylori

(V1) ORIGINAL SOURCE:

(1V) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 432 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1028:

TCTAAGTTG GCACAGAAG GCTTTAGCC ATTTAGGCG ATGAGTTAG GCATTTTAA
ATAAGGAT TGTGAAGAA TTTAGGAGT ATGGAGGCT TGTCTGCTCT TGTTTTGT
TTGATCGCTC ATTGCCCCC GTTGGTTT GAAGGCTTA ATGCTTCGA AACGCCAGC
AGTTGATCA CGATCTACT CTTGTTTG CCGTGTCTT CTTTACGC CATGCTTTG
ATTGGGTTT TTAGCCGCA GAACGAATAC AATGCGACA AGTTGGGCG GAGTTTAA
TCTAAGAGA CTTAGCCCA AGCGTTAGT TCCATGTGA ATGAATAA AGCGTTCCC
TATTCACAC CTTTTTATGT TTCTTGCA TACCGCAC CGCGGCTATT AGAAGCGCTA
AAAGCTTTG ATATGAAT TGAA

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TCGTCTCTCA TCAATAGTTT TAAAGAAGCA AAGGAATGA AATCTACAAG AATTGGTTCT
 AATAATTGTC TGAATGGTGT TCGGGGTGTT ATGTGCTATTA GCGCTGTATT GGGCGTTATT
 ATCAGCTACA AGGTGGAAG CGTGTGTCAG AGCCAGCCA CAGAAATTGCT GCAGAAAAAA
 GCTCAGTTAG TCAGTTTAA AATTCAGGC ATATGAGC GCATTTTAT GGGCGCTAAC
 ACCCTTGAA AGTTTAA GCGCTTAA CATGGAAT GCGCTTAA ATGACACCTT AAAAAAGAGC
 ATGCTCTCTG AGTTTGTGTT AGCAAAACCT CATGTGTTAT TGGTGAAGCG GATTATACG
 AATATATAG AACGATGAT CACTGCAATG AACATGAT CAAAAATCGG CTACCCCTAT
 ACCGACTCA ATGAAAAAT GACCAACCA ATCCATCGG TCAAAAGTAT AACCCGTTCA
 GATCCCTAT ATAAAGAGGT TAATGCGCAT AAATCTATG GATGGAAT TACCCCTCCC
 CTAATGGCA AGATCAAAA TGTATAGCG GCGCTGAT TCTTTTAA CATTGACGCT
 TTTATACG ATGTGCTAGC CAGAAGAAC AGCAACCT TTTAATGGG GAAAGACGCG
 TTTATTA TCAACCTTA TCGTGAAT CAGATAGA TTTAAGCGG TATCAATCGG
 GATAAAGAG TCGCTAAGC TGTGAGTAT TACAATCAA AGCAAGCGG CACTTGAAGC
 TACCATCAT TGAAGGGGAA TACAGAAAC TTTTACCA TACAGCCCTT TGAATTTT
 GAAGAAAAAG GGAATPACGG CCAATCATG GCGTTGGCA ATTGGGAAT ATGTCAA

(2) INFORMATION FOR SEQ ID NO:1030:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(14) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..303

(14) SEQUENCE DESCRIPTION: SEQ ID NO:1030

GGGTATTT ACATAGCT TCTCCACAG CCCCACCTA AAAACCCCT AACCCGAGA
 TACCGCTTT TAAAGAGAT ATCACTTAT TATGCAAGCT CTTTATTTGT ATTATTTTA
 AAAATGCC TTAAGCTTT TTAATTTG TTAATTTG TTAATTTG TTAATTTG
 TTTTGGCTCT TGGTTAAGCC TTTCTTCTAT CTTTGAAT TGGTGGCTCA TTTGAGCACT
 CCGATTGATT TGAATGATA GCATGTAAAG GTTATCATC ATCAAAAGCA CCACACACAG
 CCC

(2) INFORMATION FOR SEQ ID NO:1031:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(14) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(2) INFORMATION FOR SEQ ID NO:1033:

AAAGGTTT TACGTTAA AAGGTTAT GTTTTATTA AAAAAAGG TGAATGCTC
GTCAACTCCA AAGTCCAAC GCTTAAAGTC TTTTCAAAAT TTTTCAGCAA TTTCAAAATC
ACTAACTCA AAGCAACCA CACAAGACTT TTGAGAAAT TTGAGAAAT TACCCGTTAA
GCCCATGACA CTGAGATCAT TTAAGTCCACT TTGCAAGTGG TCCCAAGTGA TTCAATAGAA
ACCGTGGCT TTAGTTGTTT GATTTTAGCG GTGCTTACA TCTTATACA ATACGGCGGA
GCTAGAAATG TACTCCCTAC CATTTCTATG TATGCCCCAG CGCTTATCG CATACTCCCT
TCTGTACTAG GAGTATCAG CTAATATAT GAAATCCGCTT ACAACCCAGCT TGCACCAAT
GTTGTTTAA AAGCCCTTC TAAAGACCATC GTTGAAGAGG ATTAGTCCC TTAGACTTT
AATCAAAAA TCACTCTCCA AACAATTCA TTGCTTATA AGTCAAAACA CCGGTTTAA
AAAAATTCA ACCTCAACAT TCAAAAAAGT CAAAAAATCG CTCTCATAGG CCAATAGCGG
TCCGAAAT CCAAGCTGGC GATATTTAT ATGGGGCTTA CTTACCTTAA AAGTGGGGAA
ATTTTATG ATCAACCCCT TTAAACCCAG GCTCATGCGG TAAAAAATA TATCGCTTT
GGCATGCTA TAGATGAAA ACCGTTGATT AAGTGTGCA AATGGCTCA TATCTATGAT
GGGAGTCCG AAGATGAGG CCTTAAAAA CCAAGTGGCG AAGGGGGG TAACTTAGC
GTTTAGATC AAGCCACTC AGCCCTAGAC AATGAAAAA ATGCTATTC CCCACCGATT AAGCAGGATT
ATCTATCAA TCGCTAAAA TAAAAACCTA TACATGAGC CAACACAAAG ACAATCTCG C

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1032

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...1131

(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1032:

TTTATGAT GATAGAAAT CCACCCGCG GCTAAGATG GGAAGGCT TTTTATGAT
CATGGCATGG GTGCTGAT TGGCGAGAC ACAGATGAT GAGATGAT TACCATTTAT
CATGGCCGTA CTCTGGGGG TACGGGCAAG TTAAAGGCA AACGCCACC TACTTAGGC
AACCGAGTGG TACTTGGCG AGGGCTAAG GTCTTGGCG CGATTTGCGT GGGCGATGAT
GTAGGATTG GGGCTAATC GTGCTGCTT TCAGATTAC CCACGGGTC TACGGCTGTA
GGTCTAAG CCAAAACCAT CACAAGGAT CGT

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1031

(1x) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION 1...333

760

(D) TOPOLOGY: circular

((I)) MOLECULE TYPE: DNA (genomic)

(((I))) HYPOTHETICAL: NO

(IV) ANTI-SENSE: NO

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...687

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1033

GCCTATAAAA AAGCGAAT CATGCCGCTT GAAGTGCTT TATGCGATT TGAAGCGT
 AATGATTAAG AAGCGGCTT GAAGGATTT AAGGATTTT AAGGATTTT TGAAGGATTT
 TCAAGGAATG AAGGATTTT AAGGATTTT AAGGATTTT AAGGATTTT TGAAGGATTT
 GAGAATTAAG ATGCAATTAAG CCTAGAGTTT GCGGCTATCA TAGAGCAAAA GCTTTTGAAT
 AGGGGCGCAT TGAATAGCGG AGTATAGCGG TTTATGATTA AGCATTTATCA AAATTATATT
 TTCCATATCG CTTCAGCGCG CCTGCATAGC GAATTCGAAG TGTGTGCGA GTTTTGAAGG
 ATTACTAAGT ATTGAAGAG CGTTGAAGAG AGTCCCGCTG ATAAACCCCA GATTATCCCT
 AATATCATTC AAAATACCGC CTATGACCCA AGCCGTATGC TAAATGATAGC CGATAGCGTC
 AATGATTAAG AAGCGGCTTA GCGTAAATTA GTCGCTATTA CAGCAAGGTT
 TTGATTTAC AAAACTTCG AAAAGAG

60
120
180
240
300
360
420
480
540
600
660
687

(I) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

((I)) MOLECULE TYPE: DNA (genomic)

(((I))) HYPOTHETICAL: NO

(IV) ANTI-SENSE: NO

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(IX) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...495

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1034

AATAAAGCA TGCACATTT AGTCTTAATC GGTTTATGCG GAGCCGTA AAGCTCTTA
 GCACAAGAAAT TGGGGCTGCG TTTGAATAA GAAAGTCTGCG ATACGGATAT GATCATTAAG
 GAGAGGGTGG GCTTGAAGCGT GAGAGGGAT TTTGAAGAGC TTGCGCGAAG CAATTTCAGG
 AAGTTTGA AAAATTTGAT TGAATGAATTA AAAACGCTCA AAAACCCCCCA TATCATTTCT
 ACCGGTGGGG GCATTTGAT GCATGAATAAT CTTAAGGGTT TAAGGCACAC TTTTACCTC
 AAAATGATTT TGAAGACCTT GATTAGCGT TTGAATCAAA AAGAAAGGGA AAAACGCCCC
 CTTTGAATA ACCTACTCA AGCCAAAGAG CTTTGA AAAACGACACAGC CCTCTATGAA
 CTACAAATTC TCGCA

60
120
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240
300
360
420
480
495

SUBSTITUTE SHEET (RULE 26)

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1036

(1X) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...592

(V1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1V) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1036:

ATTTTAAAGCCCTTGT GATGTTAAGT AGACATATTC TCCATATATC CAAGATCCGC
ACCGATTAT AGCCCTTACT CACTTATTTG TTTCGCACA ATATCCGCAT CCACCTTCT
GAAATCAGCTT TGCATTATTT AAACAGGCAT ATCAGTAAAG TGCAGAGCTG AATCAAAATG
GCAAAAAGTT TTTTGTGTTT AGACGCTAAG GGCATGCTCA TGCCTTAAGCC AAGCCAAATTT
AAGAGCAGAG GGCATTAAGA AGGCTTATTA GAGCATGATTT TAACAGAAAG GATTGAATTA
GAATCCGATG TCACTTTTAC CGATTAAGTAT TATTTTATC AAGCCGCTGA TGAAGAGCGT
TGCATTTTAA CCGACCCCTT TCCTTCTTAA AAGGGAACG ATTTGGTACT GAGCCGCTCT
TACCCGCTGT ATGATCTAAA TAACGATCTA GCGTTGCTG TGTGCTTGA AATCCCTTTG
AGGATGCGCA TTGAATCAG CTGCGCTTCA AAGTATTTA AAATTTTAC CGAAGGAGC
ATGCTCATGT ATTTATATGAT TTCTATCATG CTCACCTTAC TGTGCTTGT TTTATTTCTG
AAATGCATTT CTAGCTTTG GACAGCGATC GTGATTTTA GCACTTTTCA CATTAAGAA
GTGTTCCACC CCACTTGTCT TTAAACCTTA GCTTAAGCCA CTTTGATTT GGTCAAGGCG
ATTTTGAAG AAGAAAGTGT GGTAAATAT AGCGGAGCA ACCACCATG GATCCACCGC
ACCATCA GCTTTTAC GCTATCATT ATCCATTAAG CCATTAAGC GTTAATGCTC
GTGTTTAAAT TCAAGCTGAG CGAGCCCGAT AAAATCACTT ATGCGGTGTA TTTGCTATC
GCGGTGCGCG TCGTTTGTAT AACCG

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1035

(1X) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...975

(V1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1V) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1035:

762

60 GAGAGTTATC AAACGGTATC TACACGCCAG AGGATTTATC AGCGGTGCTT TAGACGAGCT
 120 GTTGTAGGA ACCTGCGGT CTGTAGGTTT ACATGAGTTT ATACACAGAG GGGTGAATGT
 180 CAACGTACAG AGTAGGTTT CTATGGGGCT TACCATGGCG AGTGCTTATG ATCCCATTTT
 240 AGATTCGCA AAAACCCATTG TGGGCGAAGC CCTTTTATG TTAGCGATTT TAATTTATTT
 300 GGATTTATCG TTCCACCATC AAATCATTTT ATTTGTGAT CACAGCTTAA AAGCCGCTCC
 360 TTGAGGGCGA TTGTCTTTG AGCCAGATT AGCTAAATC ATGTCAATC CCTTTTCA
 420 CTGTGTGTC ATAGGGTTT CTATGGCGTT CCTATTTTA TCTTGCTGT TATTGAGCGA
 480 TATTATTTT GCGATGATC TGAATAACCA CCTCAATC AACCTGCTG CTATCGGGTT
 540 TCCGTTAA ATGCGATCG GGTGTGCGG CATTTATTTA ATCGCTTGGG CTATCATGCG
 592 GCGTTTAA GAGAATCA GCGTGCGCTT TACGCTTAT AGTAAATCT TT

(2) INFORMATION FOR SEQ ID NO:1037:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..1332

(17) SEQUENCE DESCRIPTION: SEQ ID NO:1037

60 GGGTTTGC GTTCTCTAT CTTTATAA TGTGCTT TGTATGAT AACGCTCTT
 120 AGTTTGAG CGTTCCGCTA CTATTCGT TCCTCTAA TCAGTCAG AAACATCA
 180 AACGAATG GCCATTAC GTTGTACC ACTATCAATG AATTTTAA TAACCTCT
 240 GATTAGAG CCATTAGAG TTACCTCTAT AATATGCT TTAGAGAAC CACATAGAA
 300 AATTAGAA AGGTTTAGC CAAGAAGCGC CACCAAGTGC ACCACAGAAA TATTGGTAT
 360 GCTAAGTGT TTAAATTCAG GATATGCTT TTATTCCTTT TAAAAAGGA TGAGCATTTT
 420 GTGCTTTA AGATTGCA TTGCGTTCT TATAGGAATT ATTCTTAGC CATACGGTG
 480 GGTATTTAT TGAATTTAT CTCTTTTAT TTGTTTTG AGAGTTTAT GCCTTTAAG
 540 GAGTTAAGT CTCAGTGA AGGCTTCGCT CAGGCGGATA AAGCGGTAG TTGTAAAGC
 600 AAGCAAAAG ATGAATAGG GATTGGCT AACGAATTTG ACAATTTGAT CCAAAAAATC
 660 AATGCGATGA ATGAATCTCG GGTTTATTT TTGCGCTCTA TCATGCAATG ATTAACCA
 720 CCTATCATA AGGCGCAAGT ACTAAGCTT ATGCTCAAG AAGAAGCTGT TTCAAAAGC
 780 TTTTCACTA TATTGATCA CTGAACATG TGAATGAGC AATTGCCCCG CATTGAGCAG
 840 CTCGCTTCA AAAATTAGG GAGCAATGAA GAAAAATTTT TAATGAGCGA TTTGATGAT
 900 AAGATTGAAA AATGCTTTT AATTGATGAA GATAAAAA GCCCTATCCA TGTATCCTCT
 960 TCAATTTACA TCAATTTAGC GATTTTGA TGTGTTGCTA TAGCGTTTAA AACCATGATA
 1020 GACAATGCGA TCAATATCAG CGATGACAAA CAGGTGTTT TCAGATTCAAT AGGGAATTAAT
 1080 TTAGTGTGT CCAATATAAG CAACCTTTA AAGAAGATT TTGAAAAATA TTGCAAAACC
 1140 TACTTAAAT CTCTTAACCC CAGCCAAACC CATGGGTTG GGTAGGCAT GTATATCATT
 1200 AAAAAAGCTT TAGAGGCTAT TGAGCTTATC ATTATAGCAA TGAGAAATC
 1260 TGTTCACCTA TCCATGATG CGTTTATAT AGTTTATC AGTTTATAGC GATTAATGAA
 1320 GAGCTACCCC CCCCCGAAA ATTGAGAGA GGTGAGGGA ATGAGGGA CAGAAAAAGC
 1332 CAATGTGGG GT

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

((i)) MOLECULE TYPE: DNA (genomic)

((iii)) HYPOTHETICAL: NO

((iv)) ANTI-SENSE: NO

((vi)) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

((ix)) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...990

((xi)) SEQUENCE DESCRIPTION: SEQ ID NO:1038

AGAAAAACA AAAAGAGAA CATGTTCAA CGATTGAGAA GATTGAGAA CAGCGAAAAA
TTAAGAGCGA TGTGAGAGA AACACGTTTA AATATTAATG ATTCAATCGC TCCCTTATTT
GTATAGAAA CGCATAGCGG TATTAAATAC GAATATGAGC ATTCGCGGAT TTTAGAAAAA
GATCACAATTG TCGCAAAAAC TACGAGAGAA ATTAAAAA GATTAAAGG TTTGATCGTT
GATCGGATTT TGTGTTTTC CGAATACACC GACCATGGGC ATTGCGGGAT TTTAGAAAAA
GCTTCGTGCT CTACAGATTA AACGCTAAG ATTTAATC TTCAAGGGCT TATTTTGGCT
GAAAGCGGTG TCGATATTCT AGCTCCCAAG AACATGATGG ATGCAATGT TTTAAGGCTG
AGAAAAAGCAC TGGATTAAGGC CGGTATTTT CACACGCCCA TCATGAGTTA TCCCACTAAA
TTTGGAGCA GTTATTAGCG GCCTTTTAGA GATGTAGCCA ATTCCTCCGC GAGTTTGGC
GATCGCAAAA GCTATCAAT GGAATTACGCT AACCAAAAAG AAGCGCTTTT AGAAAAAGCTTG
GAGATGAAA AACAGCGGTG GATATTTTA ATGTGTAAGC CGGCTTAGC GTATCTGAT
ATTGTTAAG AAATCAAGAGA TCACACTTTG CTCCCTTTAG CGCTCTATTA TGTGAGTGGG
GAATACGCCA TGTCAAACT CGCTCAAAA CACACCTGA TCACTATGA AACCGTTT
TTAAGAACGA TGACTTGT TTAAAAAGCG GAGCGGATA TGAATTATG CTATCATGCT

((2)) INFORMATION FOR SEQ ID NO:1039:

((i)) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

((ii)) MOLECULE TYPE: DNA (genomic)

((iii)) HYPOTHETICAL: NO

((iv)) ANTI-SENSE: NO

((vi)) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

((ix)) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1086

((xi)) SEQUENCE DESCRIPTION: SEQ ID NO:1039

AGCGAGGGC GCATTTGGC AGAGGATATT ATTGCGTTC ACCTTTGCC TAAATTCAAT
CAACCGCTA TGCACGGCTA TGGGTTTAA ATGCAAGACT TGGCCAAAA AACTCAAGTT
ATCCAAACA TCTTTGCCCCG GATGATGTG AGCGCTTAG AGTCAAGA AAATGAATG
GTTAAATCA TGACTGAGC GATGTCCTA AAGGATAG AAAGGATCGT TCCCATAGAA
TGCATGCTAG AGAGTCATTA AGATTCCGC CTAGCTCCTA AAGATTTTA AATTCACGCT

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 1056 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1041:

60 GGAATTACG CCTAGAGAT TAGATTAGG GAAATGCGAG TGTAAATAA GATGATAGGT
120 TTGGTGGCGG TTTTAAAGCG TTTAATAGCC AGAGACAACC CTTTGAAGCC TGAATCAAT
180 TCCAAGAAAT TCCAAGGGGG CTTAAGCGGG ATCTATGATG ACTAAGCTCA AGAATCCAT
240 GTGGAATTTG CCAAGAGCGG TAGATCTTTA AAAAATAACA CCTTCACTTA CCAAGATAT
300 GATGGCTCTA TCCATCTTAA AGTCGTGGGT ATGATTAATA GCATGATTTG GCACGTACCC
360 TTAATACTTT CCAACACAC CCTTAATCA GACGCCCTTTG AAAAAGCGTA CCAAGATCCAA
420 GATTTGATTT TTTAATGGC AAACACACAG ATGATTTTGC GTTCCCTTTA TAAATTTTG
480 CGCTCTTTG TGTATGTA TCCTTAGA ATCGTGTAG ACACGCAAAA AGGCCCTTTG
540 GATATTTATC AAAACATGGA TTTAACCAG AAGTTTTT CTACATTA AGTCGCGACG
600 CACAAGATTT ATACCCGAT CACGCTCAT TTAGACGGGA AATWACCGCTA TCTTTTGAA
633 GAAAAAAGCG GCGGTATGA ATTAATACTG AAA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1040

(A) NAME/KEY: misc_feature
(B) LOCATION 1...633

(1x) FEATURE:

(A) ORGANISM: Helicobacter pylori

(v1) ORIGINAL SOURCE:

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 633 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1040:

360 AATATCCGTC AAAAGGCGCA GAACGCTTCT TTAACACAGG TTTTAGTCCC TAAAAATACC
420 CGTTAGATTT ATGCCCATTT CGCGCTCATG AGCTTCAAG GTTCAAGA AATCAAAAGC
480 TTTAGAAAT TAAATAATCC TCTCTTAGT AGCCCGATG AATTAGTCC TTTAGGGCAA
540 AACCCCTTAG AGTCCCAAGT TTAATGATTT AATTAGATGG GTGTTTTTAA CATGCTTAAA
600 AACTACACA CGCATTTTCT AGGGGTTTAA AAAGATGATA AAAATTTACA GCTTAATAA
660 CTGAATTTG AAGCTATGA TGTATCTCTT TCAAGTGGGG GGTGAGCGT AGGGATATAA
720 GACTTTTAA AAGACGCTTT GAAAGAAAGA AACGCCCTTT TTTATTACGA AAAAGTCAAT
780 CTCAAACCTG GAAAGCCCGT AACTTTAGCC CAAGTCAATC AAAGCATTA TATAGGCTTA
840 CCGGTATATC CTTAAGTTG CTACTGTGTT TTACAGATTT TGAATCTACC CTATTTGAG
900 CGCTATCTCT TAAATAAGA TTTAATAATTA AAACCTTTTA AGGCTCAAT CAATGCCCT
960 TTAAGCTTA ATACAAAGC GACGATTTA ATCTTAGGCA ACTATTCAAA CCACCAATTC
1020 ATCTTACA ACAACCGCTA TGAATCAGGA GCGATTCAGG CCTTGCGCA AGTGGATTTCT
1080 ATCGCTTTAA TGTATGAGG AGTGGATTC GTTCAGGGCG AAATTGAAAT TTTAAGGTTT
GAAAT

765

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041

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AAAGCAGTGC CTACGCCCTCA CCACACCCCTC TTATGGCTCA GCGTGTATGA AAGCTTTAA
GAAGCCCTAG ACTTTAAGGA AGTCAATCTCA GTTGTTAGCG AATTGATTAT TGTTTATAT
CAAGCCCATT ACCCCAAAT CAAGCTTGTA AAAGCGGGGG CATCAAGCCA AGAATCCGTG
CGTAAACCTT TGAAGTAAAT TGATAGCACT TACACGATCA CAGCGAATGT GCGTAAAGGGT
TTAGCGATA TGAAGCCGTG TAAAGCGTTC TTTTAAACC TCCAACAAC GAGCCATTAT
TGATCCGCC CTACTTGCC TTGCTATGAC ACAGCGATCT ATTATACGA GCGTTTAGAT
AGAGAACCGA TCAACTCAT TCAAAACCCCG CAATTAAAGCC ACACCAAAAC GCTCCAATCA
GCCCTAAAC AAGGGGGTTT TAAAGATGAA AGCAGCGCGA TTTAACAAGC TTCCCTTAAC
TCTGTAGCT ATATGAAAG CAGTAAAGAT TTGCACAAAC TCACCACAAG CCGCGATTTA
AAGTTTTTA GCGCTTTTTT TAACCCAGCA AAGACACTT TTATAGGCAT GCGTTTGTAT
ACGATGCGT TCATTAAAGA TAAGCCTATG GTTTAAGGG GGTGTGTTT GGTATTGCGAG
TTTGGGTTTA AGGCTCATAG CGATGGCGAT GCTTTATGC ATGCGGTAT TGAATGCCATT
TTAGGAGCGA TTAAGGGGGG GATATTTGGC GAATGTTC CTGATATGA CCCCAATAC
TAAACCCCT CTCTTAAAGA GCTTTTAAAT ATCGTGTGG ATTTTCTCA AAGCATTTGG
TTGATTTGC TTGAATGG AGCGACCATC TTAGCGAAA TCCCTAAAT CACTCCCTAC
AAACCCGCGA TTGAAGAA TTGAAGCCAA CTTTGGCT TAGAAAAATC TCAAAATCAGC
TTGAAGTCA CTACATGGG AAAATGGGG TTCAATGCCA AACAGAAGG GCTGTATGTC
CAAGCGCATG TGAGCATGCG TTATAACAA AACTT

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(2) INFORMATION FOR SEQ ID NO:1042:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042

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TGCCTGGGA TGTGTTAT TCTAAAGCCT TTTTGTAGTT GTCTAAATG GCGGAATCCA
TCGCTCAAG CCGCTCTTA TCGGTTTAA AGGCTTCTTA GGGCGAGAT TGAAGACGTG
TTTGTGGGG AATGTTTAA TAGGACAATA CAAAAATACT GCGGTATTT AGAAGACAAG
ACCGCCCATT TCATGAAGC GAGCTTAAAG ACATGGCGA TTCCTTTAA TAAAGACGCC
AAAAATGATG CGGATTTGG GTTCGATTTT GCGATGGCGT TTCAAAATCAT TGAATGATTTG
TTAGACATCA CTCACAGCC CACACACTTA GGTAAAGCCCA ATTTAAGCGA TTTTAAAGAG
GGCAAGACCA CTCACCTTA CTGCTTTTA TATGAAAAAT TGAATCAGCA TGAACAAGGG
CTTTAATTT CTAATTTCA ACAAGATAGT CATGAAATCA TAGAATGAC TAAAGAAAAA
TTCAAGCAAC ATGGTATCAT AGAAGAAAC CTTAATAATC CTCAGTTTA TTCATAAAG
GCGCTTGAAG CCATTAAAGG GAAAAACAAT TTGATTTTAG AAAAACTAGC GCAAGATGTC
ATTATAGGA CTTT

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SUBSTITUTE SHEET (RULE 26)

TCCAGCAAA CAGCATTCAG GGCAGCAAG ATCATCACC CAACCGATAT TAGCGCTCAA
AAACGCCAAG AGCGGCTCGC TTCTATGGGG AAATTTTTCG CGCATTTAGC CATGAAATC
AGAAACCCCG TAGGCTCTAT CTCTCTTTTA GCTTCGGTGT TATTAAAGCA TCGCAACGAA
AAACTAAAC CCATGTTGT AGAATTGCAA AAAGCTTAT GCGCGCTAGA AAGATCATAT
AAAGCCACT TGCCTTTTC TAAAGGCAT CAAGCCAAAC GCACCAAGCA AAGTTGAAA
ACGTAGAGA GCGATTCGA AGAAGCCCTA AACTGCTACA CTACTCTAA AGACATTGAT
TTCTTTTAA ATTTTAGCA TGAAGAGGG TTTTGTACT TTGATTTAAT GGGGATGTG
TTACAAAAT TTCTGTATA CGCCATGAT GCGATGAG CCTTAGAAG GAGCGAACAA
GGTCAGGTCA AATTGAGC GTTCATTCAA AATGAATTTA TTGCTTAC CATTAATGAT

(2) INFORMATION FOR SEQ ID NO:1044:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...717
(1) SEQUENCE DESCRIPTION: SEQ ID NO:1044

AGAAAGCTAA AGATGAATAT CAAATTTTA AAAATATTAG TTGAGAGGTT ATTTTATTG
AGCTGACAG CCCATTTATG GGGGAACAA GACATAGCT TTTTAGGAT TGGTGAAGA
GCTATAAA GCGGCAATTA TTCTAAAGC GCGCTTAT TTAATAAGC ATGCAACGAT
GGGTGAGTG AAGGCTGAC GCAATTAGCA ATCATTTATG AAAAGCGGCA AGGCATAGA
ATGATTTATA AAAAGCCCT AGAATATTAT AAACCGCAT GCCAGGCTGA TGATAGGAA
GGGTGTTTG GCTTAGGGG GCTTATGAT GAGGTTAG GCAAGGCTCA AAATATTCAA
GAAGCCATTG ACGCTTACG AAGGCATGCG TTT

(2) INFORMATION FOR SEQ ID NO:1043:
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393
(1) SEQUENCE DESCRIPTION: SEQ ID NO:1043

767

600 AATGCAAGG AAGTGAAGGCT TTAATGAGC CTTTGAAC CACTAATTA
660 AAGGGAATG GCTTGAAGGCT AGCCCTGCT TGAAGCTG TTAAGCCCA TGAAGGAGC
717 ATTGGCTAT TAGAAAAATCA AGAAAAACC TTGAATTA AGATTCTTAA CGCTTCT

(2) INFORMATION FOR SEQ ID NO:1045:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...465

(14) SEQUENCE DESCRIPTION: SEQ ID NO:1045

60 AAGCTTAA CAATTTTAA AAAAGAGCTT TTGATGAAA CATTGAAT TTAAACAT
120 TTGCAAGCGG ATCGGATCGT GTTATTTATG AAGTGCAT ACTCCCATG GAATGTGAA
180 GGCAACGAT TTTCATATG GCATTAAGCC ACTGAAGAAA TTATGAAGG GTTGCAGAC
240 ATGTTGATG ATCTCGCTGA AAGGATCGTT CAATTAGAGC ACCACCCCT AGTCACTTA
300 TCCGAAGCGA TCAAACTAC TCGTGTAA GAAGAAGCTA AAACGAGCTT CCACTCTAA
360 GACATCTTA AAGAAATCT AGAAGGACTAC AAACACCTAG AAAAGCAAT TAAAGAGCTC
420 TCTAACACCG CCGAAAAAG AGCCGATTA GTTACCTTA CTTATCGGGA CGATCAATTA
465 GCCAGTTG AAAAATCCAT TTGATGCTA GAAGCCCAT TAGCT

(2) INFORMATION FOR SEQ ID NO:1046:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...393

(14) SEQUENCE DESCRIPTION: SEQ ID NO:1046

60 GGAATTCG TCGAAGAAA ACGACTTAA GCCATTCAA ACAAAATCG TCTTGATG
120 AAGAAATG AAGCGGCTT TATAGATGA TTGTTTCTA AGATTGCCCC TTCAAGAATG
180 CTGGGCTCA AACTCATGCT CGCTTTGTTA GACGAAAAA CAGACGCTAT TTATTTAGAT
240 AAAGCGCTCA ATTGTGTGC GATGTGTGAA ATGATACAGA CCGCTTCTTT ATTGCATGAT

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GATGATGATG ACAAAGGCGAC CATGCGCGCA AAGCTCCCTA GCATTAAACG TCTTTTGGG
 AATTAAACG CCGGATGCT TGGGATGCT TTTTATCTA AAGCCTTTT TGAGTGTCT
 300
 360
 393

(2) INFORMATION FOR SEQ ID NO:1047:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1731

(11) SEQUENCE DESCRIPTION: SEQ ID NO:1047

TGCACTGCTAT TTCAAAACT TTTGCCCCA ACCCTCAAG AACCCCCCAA AGACCCCTG
 TTAATAAGCC CTAAGCACCC CGGAAACGG GACACCCCCC TTCAATAAG CAGTGGGAT
 TATAATTTCC TACCCTTAGC TAAATAAGTG CTAATAAGTG TAGAAAAAGT CACGCA
 CGCATGCAAG AGCATGGGCG GCAATAATAT TGTGAGATT GCGGAGTTG
 TGGAAAAAT CAGGCCCGTT GGATTAATAC GCAAGGAAT TATGTGTTT TAAAGACCG
 TGAACAATG AATTTGTTT AAGTCCCAT TTAGAAAAA ATATCACCGA AATGCGCT
 AATTTCATCA AAGCTTACCA GCAATTACCC GTGCATCTCT ATCAAAATCC CACGAAAT
 CCGTGTGAAG ATTCGCGGTTG GTGAGAGCGGA GGGAAATTTAT CATGAAAGAT
 GGTATAGCT TTCTATGAAG CCTGAAAGC TTGATTAAG AATTTTAA CACGCAAGC
 GGTATTAAG AGATTTTAA GCAATTTGGT TTGATTTTC GCAATGTGA AGCGGATAGC
 GGGGCGATTG GGGGAGGATA AAGCAGGGA TTGTCTGTT TACACAGATG CCGGGAAGC
 ACGATCGTGG TGTGTCAAAA TTGCGATTAT GCGGCCAATA TTGAATCCG TAAACGCT
 AAAAGAACTG AGCCCTTAAT GTCCCCCAAG CATTTAGCCG AATTCGCCAC CCTAATA
 AACGCGCTC CAAGCGGTGG GAGTTTTAT AACAACAGAGC CTATTTTGT CTTAAAGCG
 CTTGTAAACA AAGTGTCCA TAAAGATAAA GAACCCCTAG CGTGTCTTTT TGTAAAGCG
 GATGACAAT TAGAAGAGAC TAAAGCCCTA AACACTTTGA ATCTTTTGG GCGGAACGCT
 TTGAATTAAG GAGAGGCCAA TGAAGAAAT TTAATTAAG CAGCGTTAAT AGCGGCGCTT
 ATAGGCGCTT ATGCGCTTGA AAGCAGATGT TGTATATTA TTTTGTATGA AGATTTAAA
 GAGCGCGATT GTTGATCTT TGGGCGTAAT TTTATGCGGT TTTATGCGGT GCGCGTGA
 TTAAGAGGCT TTGAAAAACT TGTTTATGCG GATATTTGTC AGCTTAAAG GAGCGATTGT
 TGAAGAAGAG GTTGAATAAC CATTAAGAGT TGAAGAGTGG GCATATTTTC
 TGCCTTAAT GTCAAGAGAG TTAAGCTTG TAAAGCTTG AAGGTAGT TCTTGATTA GAATGCG
 AAATCGGGG TAAAGCTTAC TAAAGCTTG AAGGTAGT TCTTGATTA GAATGCG
 GAGCGGTTTT TGAATAAGG GTGCTATGCG ATAGCCATTA GCGCGTTGCT CAGCGTGA
 TTAGAGCAAA AAGCGGATGA TCTAGGCTGT GTGTGACGA AAAATACCG TCTTTTGT
 GTGTGATCG TCGTTCTTA CCTGAAAGAT CTGAAAGAT GAAAGCCCAA AAAAAACTCG
 TATGAAAGAC TCTCTCAAA GGGCGTTGAT GCGCTGTAG ATGACAGAGA CGCTCGTTT
 GGGCCCAAGA TGAAGGATTT TGAATGATG GCGGAACCGG ATCTGATGC CTAATTTAG
 CAAACTTTAG AGAGTAAAG ATTTGATGC ATCAACCGG CTAAATTTAG AAGCAAAACG
 ATCAAGACGA TAGAATTAG AGAAAAAT TTAGAAATGT TAGCCAGCGA A
 60
 120
 180
 240
 300
 360
 420
 480
 540
 600
 660
 720
 780
 840
 900
 960
 1020
 1080
 1140
 1200
 1260
 1320
 1380
 1440
 1500
 1560
 1620
 1680
 1731

(2) INFORMATION FOR SEQ ID NO:1048:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...552

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1048

ATTGCTGAGC CAGAAGTGC AATAATGACT GCAATGATGC GTTATTTTCA CATCTATGCG
 ACCACTTTT TCTTCCCTTT GCGGCTTCTT TTGCGGTTA GTGCGCTTTC ATTGCTCTTT
 AAGCGCGCGC AAGACACTGC CGCTAAGATC AAGAAATGGG TTATGAAAAA ATCCCTTAAA
 AAGAAGAAC GATTGACTT TTATAAAGC TTATAAAGC AAAACCATAT CGCTATGCTT
 AAAAGATAG ACCCTAGAGA GTATAGGGA GCTTAGTCA TTGCGACGCC TTGTATAGAA
 ATCAACCTTG AACTAAGC CACTCAAGC AAAATCAAGA CCAITGAAAG GGGCTTTTAA
 GCGCGCTCA TCATGCTGCA TAAGGCTAAG GTGCGCATCG TGTTCAGGC GCTTTAGCG
 ATTTTTCG TTTTTTAT GTTGTTTAC TTGACGCGCT TTATAATGCT GCGTTTAAA
 GACTAAGC GCATGTTAT AAGCGTTTAA ATAGGAGCG TGTGTCTTCT TGAGCGGATC
 TATTGGTCTT TG

(2) INFORMATION FOR SEQ ID NO:1049:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1049

CTAATAAAA GCAATCAAA AAGTGGCTT TTGCTAGGCG AAGGGCGGAA TAGTGAATC
 TTGAAGCTT CCAATGCAATC GCTTTTAAA ACGATGCGG TTATTTCTAA CCACAAACCT
 ATTATCAAG AGTTTACGA ACTCAATTCG CATTAACGGCT TGTAATTATCA GCGTAAATGTC
 TTTTGGCTT ATGAATCTTG CCGCTTAGCG TTAGAAAAAG GGGGGTTAAT TTTCGATTAAT
 TTTCTAAAT TCGTGAGCCA CAGGTTGCAA

(2) INFORMATION FOR SEQ ID NO:1050:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

770

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(17) SEQUENCE DESCRIPTION: SEQ ID NO:1050

ATGCTAGAGA GCGTGAAGCT TAAATTTCT GCAGACGATA TTAATCTTA AATGTCCT
 GCGGTGATGA TTACAGCCCTC CTGCCCCCCC TTGCGCAAGAC AGCGCGATTA AATTGATATT
 CACATTTCTT CTATTTGGCGA TCGCAAAATCC ATTCAAGGAG GCACTTTAGT GATGACCCCT
 TTAATTCGGG TAGATGGGAA TATTATACCC CTGCGCTCAAG GCGCTATCAT TTCGGGTATAT
 TCTAGTACT TCGTCTCAGC CATATATCAT CACGCGCGCA CTATTGAAAG GGAAGTTTCG
 TATGATTTGT TCCATAAATA CCGCATGACT TTAAGCCCTGA AAAACCCCAA TTTTAAATAAC
 GCTATCCCAAG TGCATAACAC TTTAATATAG GTATTGCTA ATAAAGTAGC CATAGCGCTA
 GATCCCAAA CCAITCAAT CACCCGCCCA GAGCGTCTT CTATGCTGA GTTTTATGCT
 TTAGTCAAG AATATCCCAT TTAATCCCGC GCGAATAATA AGATCAATTGT AGATGAATAA
 TCAGGACAGA TCGTTTCAAG AGTGGATATA ATCTGCGATC CTATAGTGT TACAAGCCAA
 GACATCACGC TTAATATCAC TAAAGAGCCT TTAATGAT TTAATAACAT GCAAGATTTA
 GACATATACA TGTCTTAGA CACCGCTCAC AACACGCTGA GTCTAAACGG GAATAAACATC
 ACCATTCGCC GGTGGTAA AGCCTTACAA AAAATTGCG TGAGCGCTAA GGGGATGCTT
 TCAATCTTGC AAGCCCTTAA AAAAAGCCGC GCGATTAGCG CGAATGAG ATACTATGAT
 AAACAACAA

(2) INFORMATION FOR SEQ ID NO:1051:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...666

(17) SEQUENCE DESCRIPTION: SEQ ID NO:1051

ACGGACATC GCAGTTAGG GTGATATTA AATCCAAGA AGCCCAAGTT TATCGACTA
 AAACAAGCCT GATTTATGA GCGCATGCTA TCTTTATGA GCGCGTTGA TAAAGGGGC
 GTTCAATAC GCCTTCTAC AGCTTGTGA CTGCTTTTA GTTGGCTT GCCTTAAGAT
 TTAGAAATCC AAACCTTTGT GCGTAAATAC CTTTCTTAAA ATCAAAAT ACAAGCCCTA
 CAGGAGCAAA TTACGCGCTT AGATTCTCA GAAAAAGTCTG TTAGCAAAATG GATTAACCCCT
 ATTTTGTAT TAGGCTATTA CACGCTTAC GTGAGCGGAT TTTCAGGCT GATTAAGCAC
 TTATGCAAA ACATAGCCTT GGGTTTGTCT CAAAAAGTGG ATTTAAATG TAAAAAACTC
 ACCGACTCA AATGATCA TTAGAAAA TTTAGAGCT TAAAAAAACC

771

540 AACGACCAAT TGTGATTA TTAATGATA AACGACATG AAAACTATTA AAAACCAACA
600 GAAATAGAGC TTTTAAACAC AGCGATTAA AATTAGAA ACACCCCTTA TCAAGCCAAC
660 CATTCAGTT GCGCCGATTT AATAGCGATC GCCAAGTTAG AAATTTTAA ATCCCAATTA
666 GAAATC

(2) INFORMATION FOR SEQ ID NO:1052:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(14) ORIGINAL SOURCE:

(14) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..1041

(14) SEQUENCE DESCRIPTION: SEQ ID NO:1052

ATGCTTTTC ATCAAGGAG TTGAGCGTG AGCGGTTTG TTAATAATCG TATTCGTAGT
120 TTTAAAGAA ATAAAGCGCG GGTGTTTTC GCTTAATCTT TTAATCGGCTT GTTACCGCTT
180 TCTCTTTAG CCCCCCTTGT GGTCAATGAT CGCCCTTTAT TCATCTATTA AGACAATAAA
240 GCGTATTTCC CTATGTTTAA AACTATAGCG GAAATGAGAG TTGAGAGCGA TTTTTCACAC
300 CCTACGAGCT ATACGATCC TTAATGACAA AACACGCGTT TAAAGACGCG TTTCATCATC
360 CATGCGGCTCA TCCCTTAAG CTACGATACG ATCATATATG ATTTAGACTC GCCTGCCCCC
420 ACCCCCCCA GCTTAAACA CCTTTAGGC ACAGACGATC AAGCCAGAGA CGTGTTAGCC
480 AGCCTGCTTT ATGCTATCG GGTTCGTTA GTGTTTGGG TTTTACTAC CCTTTTAGC
540 GTTCTTATG GCGTACGTTT GGGGCGGCTT CAGGGGTAT TATGAGGCGT AGTGAATTTA
600 GTGGGCGAAA GGTTCAGGAG AATTGAGAG CGCATCCCCA TGCTTTTCTT ACTCATTTGT
660 ATTTCTAGCG GGTTCATTC TAAATTTTG ATCATCTTGT TTTTAGCTT GCTCTTTAGC
720 TGGATGGGCG TTCTCAAGT CGTGCGCACG GAGTTTTTA AAGCAAGAA TATGACTAC
780 ACCAAGCCG CTAGAGCGCT TGCGGTGAT GATTTAAAA TCATTTCTA CCATCTTTA
840 CCCAAGCGCT TAGTGGCAAC GATCACTTAC ATTCCTTTT TAAATGCGGC TAGTATTTCC
900 ACTTTAGTGT CTTTGAATTT CTTAGGTTT GGCATGCTTA TAGGAGCGG GAGCTTGGGC
960 GAATGGTCA ATCAAGCAA GATTAACCTC ACCACGCCCTC AATTAGCGGT TGTAGCCCTT
1041 TTCAAGCCTA ACATGCTCA A

(2) INFORMATION FOR SEQ ID NO:1053:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1557 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(14) ORIGINAL SOURCE:

(14) ORGANISM: Helicobacter pylori

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1056

(B) LOCATION 1...1098

(A) NAME/KEY: misc_feature

(1x) FEATURE:

(A) ORGANISM: Helicobacter pylori

(v1) ORIGINAL SOURCE:

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 1098 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1056:

CTGAATTCA GCGTTTAC CCTTCCCG CACTCATCT TCCCTTATT TGAAGATTCT
 ATTTAAATA GACCGTTAGA AAAAACCCTT TTGAATTGC AAGTGTATA CCTTAGAT
 TTAGCGGCTA ACAAATATCA AAAAGCGGAT CACACGCTCA TTGGTGGGGG TGCGGGGCAA
 ATTTAGACC CTGAGATGAT AGAAAACGCA CTCACACTCTG TTAATAAACCC TAAACACACG
 ATTTTTTAA GCGCGGTTGC CAAGCCCTTTC AAGCAATAG ACGCGATGCG TTGGCTCAA
 AAAAGCATC TCGTTTGGT GTGCGGCGCT TTGATGACG CTCTATTGAA CTCTATTGAA
 TTGGTGTCTG ATGAGGTTT TTGTATAGC GATTATATT TAACAGGGGG CGAGCTTGGG
 GCGTGTGCT TGAATAGTAG TATCGCTGCG CACATTCAG GGGTTTGGG TAAACGCCCA
 TCTTTAGAA ATGAGAGTT TGAATAAT TATTGAGA CCCCTAATT CGCTAACGCT
 GTTTTAAAT CCAAGAAAT CAATAAATC CCTGCACCTT TAGAATATT TAAAGGAAT
 CATGCTAAA TCAGCAACT AAAGCTTGAT TTGCAAAAT TAAGACAAA ATTTAACCGC

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1055

(B) LOCATION 1...687

(A) NAME/KEY: misc_feature

(1x) FEATURE:

(A) ORGANISM: Helicobacter pylori

(v1) ORIGINAL SOURCE:

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 687 base pairs

(1) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1055:

ACTCCAGAT ATAGCATTA TAACACCAA CACTCCAG CTCAAGTAC ATGAATGTG
 TTAAATGGCT TTAGCAATGT GAATATATGT AAAGAAAAGT CTCGAGTAC CGATCCACTG
 TGGCTAATT

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1701 base pairs
(B) TYPE: nucleic acid

(2) INFORMATION FOR SEQ ID NO:1058:

AGGAAAGCGA TGAACACCCA CCTCAACAAT TGATTTGAAA TTTCGCACTT GATTAAGAAA
ATTGACTCTT TAGAGCCGCTT GATCAGAGAGG AATCGGGAAG ACTTTGTAAT AGCCTTGAAT
GATTAAGAGAG CTAAATAATA AGCGATTCTG AATTTGGAAG AAGATAAATT AGCCTTAATA
TTACAGGTTT CTAAATAACA GCAATCCCTA CAGAAGACAGG AGCCTTAATAAT CGCCAGTATC
CAAAAGAGAT TGAAGCGATC CAATCAAGCC AACAAGAGAA TTGATAAACC CTAAATAATGAA
GATATTGCTA AAGAGCGATC CAATCAAGCC AACAAGAGAA TTGATAAACC CTAAATAATGAA
ATCAAGACCA AAAAGCCGAA ACAAGAGATT TTGATAAAGG AATGCTAGA GCTTGAATAA
TTAGCCGTTG AATTGAGAAA TTGAGTGAAG AACGAGATCA AAAACATCAAG AAGAAACCCA
CAGATCATCT TTAATAAGAA AGAAGAACTC GTGAAAAAAA CCGAGCCTAA AATCTATAGC
TTTATGAAA GATTTAGAGG GTGGCCGAAA AACACGAGCA TCGTAACGAT CAAAAAAGAG
GCTTGTCGGG GTGTTTAT TCGGTTGAAC GATTAAGATT ATGCCGAGT GCTAAACGAGT
GGGACATGA TCACTGTCG GTATTGCGGG CGTATTTTAT AGCGTAGAG TACGCATGAA
AGTAACGCTC AACCTCCAAA AGAAAGCCAA CCAAGAGAAA GCCAAGAGAG AAGCCAAAGAA

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1057

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...810

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1057:

AGGAGGAGAT GATTTCACCT TCGCTCAACG CCCCCACCG TGGTTTAAT GCGAGTTTG
CAAGGGAGCG GGAAGACAA CACCAACCGCT AACCTCGCC ACTATCTCA AACCAAAAT
AAAAAAGTGC TTTATGCGC ATGCGATTTC CAGCGCTTAG CAGCGGTGCA GCAATTAAAG
GTTTGGGCG AACAGGTGCG CGTGAAAGTT TTTCATGTAAG AAAATTAAG CGTGAAAGAA
ATCGCCACA AGCCTTAAG AAGGCTTAAG GAGCGCTAAG AATCGTGAT AATCGTGAT
AGCGCGGCG GTTAAAGAG CTATAGCAG AATTAAGAG AGTTAAAGAG AGTTAAAGAG
GTTTAAATC CCATGAGAT GCTGATGTC GAGAGACCGG TGAGCGGCG AGATGCGGTC
AAGAGTGCAG ACACCTTAA TGAAGAAATG GCGGTGAGCG GGTGCTGTT AAGCAAAATT
GATAGCGGAT CTAAAGGCGG TATCGCCTTA GGCATCACTT ATCAATTGGG CTAAACCTTG
CGTTTATG GAGTGGCGA AAAATTCCTT CATTTAGACG TGTTATGCG TGAAGGAT
GTGGGCGCTT TGAATGGCG TCGATATAT ATCTCGCTCG CTGAATAAAC CGCCAGCGTT
TTAAACCTTA ATGAAGCCAA AGATTTAAGC AAAAAAGCTCA AAAAAAGGCA ATTCACCTTC
AACGATTTT TAAACCAAT TGAAGAGTG AAAAAAATAG GCTCTATGAG TTCTCTGATC
TCTATGATTC CAGTTTAGG GATATGCGA AGCGCGCTTA AAGACACGCGA TTAGAAAGT
TCTTAAAG TGAATAAAT CAAGCGCATG GTTAATTCCA TGACGAAAAA AGAGCGAGAA
AACCCCGAG TTTAAACCG CAGCGCAAG AAAAGGATC CTTAGGAG CGGCTTAGAA
GTGCTGAAA TCAATCCAT CATCAAAAGC TTGATCAG CGAGCAAAAT GCGCAAAACGA
CTCAGCAAT TAAAGGCTAT TACGATTTC ATGAATCTAA TGAATCAGC TAAAAATCAA

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1..1701

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1058

[illegible]

(2) INFORMATION FOR SEQ ID NO:1059:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOP SECRET : INTERNAL

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(2) INFORMATION FOR SEQ ID NO:1061:

ATGATGTCAT TGAAGCGTC GTGTTAAGA TTGATGGCGG AAACCAATAC CGATGATTTA
AGCCACGCGA CGACGCGCTT CACACGAGAG GATATTCCTT TACACCGCAA AGCCATGCTA
AAAAACCGGA TTCAAAATTA CGAACACCGC ATTGAAGCCA TTAAACACTAA AGCGCTCCT
GTACCGTATG TGGCGCATGT GGTGGCACA GGAAGCTCTA GAAAAACCGC GACTAACTCT
ATCATGTGCG ATTTGTGTAA GACATTCCTT TTGTGCTCTA ATAAAGGAG TGGAGCCATT
GTGATTTGGG GGGTGTATCG TCCGATTTTC TTGCGACTGT GTGAAGTAG CCGGCGCTTA
CCCATTTGTC CTGATGTAA GATTTGAAA GAGCGCGATA TCATTAAAT CTACCCCTTAT
AAAGCGCGAA TCACGCTGAA CGATTAAGCTG GTTACGACCT TTAAAGCTAGA GCTTGAACCT
TTATTAAGATG AAGTACGGCG TTCTGGCGGT ATCCCGCTTA TCATTGTAG GCGTTGACCC
AATAAAGCGC GTAAATTTT AGGCTTAGGC GATTCGGAGC CGTTCAAAA ACCATCCGCT
CCTAAAAAGC AGCTTAAAGC CTACACTTA GCCCAAAAA TTGTAGGCCA TCGTGTGCGG
GTAAAAAGGA TCTTACCTGG TGCTTATTTGT GAGCCAAAAG TTACCAACCGT GGGCAGTCAA
GACACCAACAG GGGCGATGAC CAGAGATGAG GTTAAAGAT TAGCGAGTTT GAAATTTGAT
AGCGCTTTTG TGTTCAGAG TTMTGCCAT ACCGCTGCTT ACCCAAAAC TAGTGTGTG
AGTTTGATG CAACTTGCCT TGCTTTATC ACTCAAGAG GGGCGGTGGC GTTCATTCG
GGCGATGCGG TGATCCATAC ATGGCTTAAT CGCATGGAT TCGCTGACAC TTAGGCACA
GGGGGGGATA GCCACACCGG TTTCCTTTA GGCATCAGTT TCCGGCAGGG AGCGGGC

(*) SEQUENCE DESCRIPTION: SEQ ID NO:1060

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1017

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1060:

GTACATCA AAACCTTAT TAATGATTA AGAAGGATC ATGACAGGCA AGATAAAAA
CAAGCGGTT TTGCTGAAT TTCTGGGA AGCTTACCT GGGGACAAAC AGTTGATTT
GACATCATG TGTAGATCA CATCGCTAAA GAGATCAGAA GTTGTAGTGA AAACGATATT
GAAGTGGTAT TTGTGATTTG TGAGAGCAAT ATCATTTAGGG GCGTTAGCGC GCGTCAAGGG
GGATCATTA GCGGACCCAG TGGGCAATTAT ATGGGATGT TAGCCACCGT GATTAATGCG
GTAGCATTC AAGAAGCTTT AGAGCATATC GATTAGACA CAGAGTGC AAGTGCCATT
GAAATCAAG AGATTTGTGA AAGTTATATT TATAGGAAG CGATCAGCA TTAGAAAAG
GGTAGGTTG TATTTTTGCG CGCTGGCACA GGAACCCGCT TTTCACCGC CGATACCGCC
GCTACTTAA GAGCGATTGA AATTGATCG GATCTAATCA TTAAAGCGAC TAAAGTGAT
GGCATCTATG ACAAAGACCC TAACAAATC AAAGAGGCTA AAAATTGAC ACTT

(*) SEQUENCE DESCRIPTION: SEQ ID NO:1059

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

((i)) MOLECULE TYPE: DNA (genomic)

((iii)) HYPOTHETICAL: NO

((iv)) ANTI-SENSE: NO

((vi)) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

((ix)) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...462

((xi)) SEQUENCE DESCRIPTION: SEQ ID NO:1061

ACATTTACTA TAAAGAGATT TGTTCGATG AAAATTAAAT TCCAAAAAAT CCACCCAAAC
GCCCTATCC CTAAATACCA AACCCGAAGC TCTTCAGGCT TTGATTTGCA CGCTGTAGAA
GAAAGTAGTA TCAAACTCA TAGCGTAGGA TTGTAAGGA TTGCGATTG TTGTCCTTA
GAGTGGGGGT ATGAACCTCA GTTACCGACC CGTAGCGGCT TGGCTTTGAT TCATCAGGTG
ATGGCTTAA ATTCCTCG CACGGTGGAT AATGATTAAT GGGCGGAAT TAAAGTCATT
TTAGCGAATT TGAGCCGATA AGATTTAA GTTCAAGTAG GGATAGGAT CGCTCAAGGG
GTGGTTCAAA AAACTTATA AGCCGAATT ATAGATGCG AACAAATGAG TGAACCTCA
AGGGGTAGCC GGGGGTTGC CAGCACAGCA GTGAGTAAGC CA

((2)) INFORMATION FOR SEQ ID NO:1062:

((i)) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

((ii)) MOLECULE TYPE: DNA (genomic)

((iii)) HYPOTHETICAL: NO

((iv)) ANTI-SENSE: NO

((vi)) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

((ix)) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...525

((xi)) SEQUENCE DESCRIPTION: SEQ ID NO:1062

AGAAAGAAC CATTCAGGA ACCGATGAT TTGATGATA AACCATTTT AATCTTACTC
ATAGCCCTTA TGCCTTAG CGGCTGTAC ATGAGAAAT ACTTCAAAAC CGCTAAACAC
CAAAATTAAG GCGAAGCGTA TTCCCTTAC CATTTGCAAG AAAGCATCGT TTCGTCATAT
CGTATGAGC CCAATTTGAA AAATGAGCG GTTATAGCG ATAAAGGTT AACGCAAGTA
AGATTTGCTA AGATTTCA TTATGAAAGC AGTTTTTA ATGAGAGTCA AGGTTTTTC
ATCCTTGCA AGATTGTT GAACAAGATT GATTAATAA CAAGCAAAAG CAGGGCGGCT
AAGCTGAGC AACCGAATT GAAATTAAG GCGCTGAAG CGGAAGTCCA AGATTAAGTC
TGCTATCAAG TCGAATGAT TAGCAATAC CTTAACGCCA GCCAACATC TATCGTTATT
CCTTGAGAG CTTTGCCCTT GCGCGAGCG TTAAGGGA TCTTT

((2)) INFORMATION FOR SEQ ID NO:1063:

SUBSTITUTE SHEET (RULE 26)

AACCCCTATA AAAAGGCTGA GCAAGATAA AAAAAGGAT ATAAATGAT AGTGGCTTTC
 ATAGGGGGTTC TCGAATAAAT CTCTGCTTTA GAAAGGCTTA TAGAAGTGCA AGGGGTTGTT
 120
 180
 180
 240
 300
 360
 420
 480

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1064

(B) LOCATION 1...594

(A) NAME/KEY: misc_feature

(ix) FEATURE:

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 594 base pairs

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1064:

GCGATGAGCA TTAAGGAAA TTAAGCAG GTTAAGAAC CATTTAAAG CGATGAAAAG
 CTTTGAAG GAGCGTTTTC ATTAGAAG TTTTCAAG CTTACAGTG GGTGTTGTTG
 120
 180
 180
 240
 300
 360
 420
 480
 540
 600
 657

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1063

(B) LOCATION 1...657

(A) NAME/KEY: misc_feature

(ix) FEATURE:

(vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

(C) STRANDEDNESS: double

(B) TYPE: nucleic acid

(A) LENGTH: 657 base pairs

(i) SEQUENCE CHARACTERISTICS:

540 GCCCTAGAGA GTTGGGCTT TAAAGCGCT GAAATCAATC CAGTTTAA AACCTAAAA
594 CCCCATCTCA GCATAGAGC AGCGATTAA GAGGCCCTTAC AGCAACTGCG CTCT

(2) INFORMATION FOR SEQ ID NO:1065:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..1221

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1065

AGTCGCACCC TTGTGCATA AATCGTTTA CAAAAGAAA GGAAGAAAAT GGAATATCAA
CAACACACCC GCAAAATCAA TCGCCCTTTA GTTCTCTCG TTTAGCAGG AGCGTTGATT
120 CAACACACCC GCAAAATCAA TCGCCCTTTA GTTCTCTCG TTTAGCAGG AGCGTTGATT
180 AGCCCATATC CCGAAGAGAG TCATGCGCCG TTTCACAG CCGTGATCAT TCCAGCCCAT
240 GTTGGGGGGT TCGCCACAGG CACTGCTGTA GGAAGGCTCT CAGGCGCTTCT TAGTTGGGA
300 CTCAAAACAG CCGAAGAGAG GAATTAAC CCAGTAAGT CCGATTAAGT TTGGCGCAT
360 CAGCAGAG AAGCGCTTTA TGAATTTCTT ACGACTTATA CAAATCCCTT
420 TATCCAGTA AGATTGATCG AGTTGGGAC TGGGGGAAAG CCGCTAGGCA TTATTGGGTC
480 AATGCGGGGC AATGGAACAA GCTTGAAGTG CATATGAAAG ACCCTGTAGG GACTTATAA
540 CTATCAGGCG TTAGAAACTT TACTGCTGGG GATTAGAGG TGAATATGCA AAAAGCCACT
600 TTGCGTTTGG GCCAATTCAT TGCATTCCT TTCAAGAGT ATAAAGATAG CGCTGATCGC
660 ACCGAGAG TGAATTTCA CCGTAATAAT ATTCAATTG ATATTTTGT AGAATCAAT
720 AATCGTGTG GTTGTGAGC CGGAGAAA GCCAGCTCTA CGTTTTGAC TTGCAAGCT
780 TCAGAAAGGA TCATTCAGC TAAATTTCTG GAAATTTCTC TTATGATG CGCCACGCTC
840 AATTGCGCTT CAAACAGCGT TAAATTAAT GGAATGTTGT GATGCGCGG TTGCAATAC
900 GTGGAGAGCGT ATTAGCCCC TTCAACAGC ACGATCAACA CTCAAAAGT TCAAGGGAA
960 GTGATTTTA ACCATCTAC TGTGGGGAT CAAAGCGCGG CTCAGCGCGG CATATCGCT
1020 AGCAATAGA CTCATATG CACACTGAT TGTGCGCAAA GCGCGCGGTT AAATATCAT
1080 GCGGCTCCAG AAGGTGCTA CAAAGATAA CCTAATAGTA CCATTCTCA AAGTGGCACT
1140 AAAAAAGAGT CAGTCAAAAT AACATAGCA ACACAGAGCT CATTAACCA
1200 CCAATACA CGCAAAAAC AGAACTGAA CCCACCAAGT CATGTATGG CCTTTGCTG
1221 AAGCAAGA CTCGGTGTG A

(2) INFORMATION FOR SEQ ID NO:1066:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

600
540
480
420
360
300
240
180
120
60

CCGCAAT TTGAAGTGG CAGAACAAAT AACGCCAAT AAAAGGGGGT GGTGATGGAT
TCTTATAT GTATTAGAG AGCGATTG CTTTAAAGCG GTGAATTTT AACGCTTTT
ATTAGAGGGT TTAACAGCC AGAAAAATTT GATTAGCAC TTGTGATGT GAGCTTTAT
ATGCAATTA AGTGAAGTTT GAAAAACGAC CAACGCATAG AATGTTACGA AGAATGCGAT
TTAGTCAAG TGGCTTTT AAAAGGGGGT AAAAGGTTG TTGCGTGA TGTGGGAAA
GATCATTTA TAGATTTA AGAAAAAGTT GTTTAGATG TGGAGCGAG TAAGGAGAGC
CTCATCGCT CCAATCTAT CTTAGCAGG GCTGGGAAA AATTAGGCG TTTTAAAG
GTCAATAAAA TGTGTGTTT TAAACCTCT TTATCTGTA AAGAGGGCG TCAATTCGA
CAGCATTAG CAATAGCAG AAAAAAGCT TTTTAAAG TTTTAAAG AACGCTTTT
TTGCGTTAC CAGTCCCT TACTCAAT TTATGCGC TAGATTACG CTTATTCAC

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1067

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...738

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1067:

1278
1260
1200
1140
1080
1020
960
900
840
780
720
660
600
540
480
420
360
300
240
180
120
60

GTAAATATA CACTAGTAT GTAAAAAA ATATTTTA CCAACACTT AGGATTTA
TGTCTAGGA TTTTGCTT TTACGGGAT TTAATGATG CCAATATCTT AGGGCTGG
GTGTATAGG ATATTTCTT TGTGCTTTT AAATGCTTA ATCTATTCAG GCGTATTTT
GCTGAGGGCT CTTTCTTCA AGCTTTTTA CCGAGGCTTA TACGAGTTT CATTAAGGG
GGTTTGCGA GTTTGTTGG GCTTATTTT TGTGGCGCTT TATTCATGTG GTGCTTAT
GTAGCGCTCA ATCCCTTAG GCTAACCA CTCCCTAGCTT AGGCTTTGA TGAAGAAAG
CTCAAAACTAT GCACCCCTAT TGTAGCGATC AATTTTGTG ATCTTTATG GTGTTTAT
ACCACTTTT TAGCGCGCT TTACATATC AAACACAGCT TTTTGGCAG CGCTTATAG
GCAGCTTAC TCAATTTAT CAGATTTTA GCGCTTTGA TTTCTTAAGA AAAAAGGCT
TTAGAAGCGT TGTATTTAT GAGCTATAG GGTCTTTAG GGGCGTGGC TCAATCTTA
TTACACTTT ATCTTAGT AAATTTAGG TTATGGGAT TATTTATTA AGGTTGTTG
GTTTAAAG CTAATAATC AAACAAAA GAATATCTG TGAATAGCG TAAATAAGAT
CTTAAAGCGT TTTTCAAGC ATCTCTCC AGCGTTAG GCAATCTAG CGCTCAGATC
GCTTCTTT TAGACACAC AATCGCTCT TTTCTGCGA GCGGAGCGT GTCTTATTTG
TATTACGCA ATAGACTCT CAGCTCTCT TTAGCCTTAT TCGCTATCCG TATCTCCAC
GCTTTTCC CTAGCATGC GATCGCGCTT AAAACACACC AGCAGATTT AATCTTACAA
CGCTTGCAAG AGCGGTGTT TTTTGTG GGGGTTTGC TTCTTTCAG CATTTGGGG
ATATGTTTA GCAAGAAAT CACCAACTT TTATTTGAAG GGGGCAAT TTAGCCCTAAA
GACACCTTA TACTTCCGA AGTCTTTT CTTCTATCTT TAGGCTTTG CCGTTTGGG
CTAACCAAC TTTTCTTT ATGCTTTAT AGCAATTAAG AGCAAAAA AGCGCTTAA
ATCTCTTAA TTTGCTTT TTACGCTTT TTAGGTTA GCGTTTGT

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1066

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(A) ORGANISM: Helicobacter pylori

780

738
720
660
AAAGAGGCCA TTTCGAACG TTACAAAAC TTAAAAAC ATTTAAAAC AAAGCATTTT
CAATCTTA CGATCCAGA AAGCTTAGTC AAAGGAAAA ACGGGAATGT TGAATTTTTT
ATCCATTTCA AGCGAGCC

(2) INFORMATION FOR SEQ ID NO:1068:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1X) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1..2547

(B) LOCATION 1..2547

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:10668

2220	AGACATGTC	AACCCGATGAA	ATCTAAAGAA	CTTTATTTAG	CTTTAATCAT	AGCGGCTTTA	60
2160	TTAGCGCTTT	TTAACCTTATC	TTCAATGCTATC	GTTCATGTTGG	GTTCAGTTGGG	GGCTTTTGGG	120
2100	TATTTGGCGGT	GGGTTTATAT	TATTAAGGCTT	TTTGGGTTATC	TTTGGGTTATC	TTTGGGTTATC	180
2040	TTAGAAAAA	CTTTAAGGCTT	AGGCGCTTAA	AGGCGCTTAA	AGGCGCTTAA	AGGCGCTTAA	240
1980	CTGTGTAATC	TAAGGGGAAT	CGGCAACAGC	CGGCGTTTGT	TTTTCACACC	TTTATATAGG	300
1920	GACTTTGGGC	TTTATGTTGCT	GATATGCTGT	ATGTTAGTTA	TCCTTATATC	AACTTTATATC	360
1860	AAACTTCCGC	TATTAAGGCTT	TTTAAAGGCTT	TAATATGAGCA	TAATATGAGCA	AAACATGAGCA	420
1800	GAAGTTTACA	TACATATGCTT	AGGCGCTTAA	AGGCGCTTAA	AGGCGCTTAA	AGGCGCTTAA	480
1740	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	540
1680	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	600
1620	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	660
1560	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	720
1500	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	780
1440	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	840
1380	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	900
1320	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	960
1260	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1020
1200	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1080
1140	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1140
1080	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1200
1020	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1260
960	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1320
900	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1380
840	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1440
780	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1500
720	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1560
660	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1620
600	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1680
540	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1740
480	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1800
420	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1860
360	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1920
300	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	1980
240	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	2040
180	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	2100
120	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	2160
60	TTGAAAAACA	CCCATATCAGA	TTCTCAAAAA	AAAGAAAAACA	ACAACACACA	AGAAAAAGAA	2220

2280 GTGCGCTTC ATGCCCCCTT TGCCACTGAA GATGAATCA AAAAATCGT GATTTTAT
 2340 AAGACCCCAA ATACGATGAA GATTCTGC TAGAAGATC GCGCATGCT
 2400 TTAGACACCC CTAACTATCA AGCGATGAC ATTCTAGAAA GGGCTAAGC GGTGATTTA
 2460 GAAAAAAGA TCACCTCTAC GAGCTTTTA CAAGCCCAAT TAAATAATCGG CTACCAACCA
 2520 GCCGCCACA TTACTGACGA ATTAGAAGCT CAAGGCTTTC TATCCCCAAG AACGCCCAA
 2547 GGCAACAGAG AGATTTGCA AAATTTT

(2) INFORMATION FOR SEQ ID NO:1069:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(41) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..1344

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1069

AATTACCTAA AATTTCATG TTCAGAGATA GCCATGACC CCAGATTCA ACCCGCCACT
 AAAAAACCT TAAATCCCT TTAGCCGCT AGTTACGCC ATTAGTGA ATGGTATGAT
 TTTTACCTT ATGCTTCTT TCCTTCTTAT TTGCGTAAAG AATTACCCA CACCAATGAC
 CCTACTCTAG CGCTCATCTC AGCTTTTGA GTTTTATGC TAGGGTTTTT CATGCCGCCCT
 TTGGGAGTGT TGTTTTTGG TAAATTGGG GATTAAGAAG GCGTAAAC TTCCATGGTG
 TATTCATTT TCTTATGCG GCTAAGCTCT TTCAATGCTC CATTCCTCC CACTAAGAA
 ATCGTAGCGG AATGGGCGGT CTGCTTTTA TTGTTAGCA GCGTTTAC GGGCTTTAGC
 GTGGAGAG ATATAGCGGT GATCGCCACT TATCTCTCTG AATTAGGCAA GAATGGTAA
 AAGGTTTTT ATGCTCTTT CCAATATGTA ACTTAGTG GAGGGCCA ACT CTTAGCTATT
 TTTTGCCTC TATCGTTGA AACGTTTAC AGCGTTTAC AATCAAGCGG GTTTGCTTGG
 CGTATTTAT TCGCTTTAG GGTATTTA GCGTACTCT CGCTCTTTT GAGAAATATC
 ATGAGAAAA CTATGATTA TGAAGCGACT CCTCAAAA AGACTAATGT AATAATACA
 AAGAAAACT ATATCAAGA AACCCAAAG GCGAGTTAA AGAATTGCT CAACCATAA
 AAAGCCCTAA TGAATGCTT TGGGCTTACT ATGGAGGA GTTGTGCTT TTACACTTTT
 ACGGTGAT TAAATATCT TTAAACCAAC AGCTCATCGT TTAGCCCTAA AGAAAAAGCAGT
 TTATCATGC TTTAGCGCT CTCTTATTC ATCTTCTTAC AACCCTTAT GCGGATGCTT
 GCGGATAAA TCAATCGCAC ATGATTTTG CGATCAACAG GCTTATTGA
 ACCCTTATG TCTTTATG TATCAAGCAT GCCATGCGG TGTATGAAGC CCTATTTAT
 GAAATACTCG CATGAGCAG CATGAGTTT TACACTTCA TTGCTGGGGT TATTAAGCGC
 GAAATATCC CTGAACATGT GCCAGCGGCTT TAGCTATGC GATCGCCAA T
 GAGGGTTTG TGCGCTATGT CATGTAGAGT ATGTTAGCT TATGGTAT GGTATATCA
 TTCCCTAAAA AACCTATT GGAG

(2) INFORMATION FOR SEQ ID NO:1070:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1938 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1071:

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1070

(A) NAME/KEY: misc_feature
 (B) LOCATION 1..1938

(1x) FEATURE:
 (A) ORGANISM: Helicobacter pylori

(vi) ORIGINAL SOURCE:
 (iv) ANTI-SENSE: NO
 (iii) HYPOTHETICAL: NO

AAATGGAATA ATTGATGCA ATTGATGCA GCTGATTTAG AACGATTAA AAGCATGCGG
 AACGCGCTTC GCTTTTGTG TGCGGACATG ATAGATAAGG GCAATCCACG
 GTGTGTTTAC GGTGATGCTG GTTAAAGCT TGCACCTTCA CCTAAACCCC
 ACCAACCCCTA AATGGCTCAA TAGGGACAGG TTGGTTTAA GCGGAGGCGG
 TTAGGTATA GTTGTGTTGA TTGTGGGGG TTGATTTGA GTTAAAGCGT
 TTCAGGCAAT TACACTCTTA AACCCACAGA CACCCTGAAT TACACCCACAC
 GAAATACCA CAGCGCCCTT AGGGCAAGGT TTGCTTAACG CTGTAGGCTT
 AGCCATACG CTCAAAAACC TTAGATAAA GAGGCGAATT CTCATAAGT
 CTATTGCTG TAGCATGCG CTGTAGGCTT TAGCATGCG CTATTGCTG
 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1860 1920 1938

AAAAAGGTTAC TCAACGCA
 AAGGCGGAT AACTCTTTGA AAAATTGCG TTAGCGTTC AAAACATTAC CGCTCAAGCG
 1938 1920 1860 1800 1740 1680 1620 1560 1500 1440 1380 1320 1260 1200 1140 1080 1020 960 900 840 780 720 660 600 540 480 420 360 300 240 180 120 60

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

GGAATGATAG CGCTGAATTT CAACTCTTA GATAAGAAA CAAACACGCC CTTATTGAA
AAAAAGCCCG TAGATTCAG CTTAGAGCTA TATAAATA GCGAATTTCA CATGCTCTAT
120
180
240
300
360
420
480
540
600
660
720
780
840
900
960
1020
1080
1140

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1072

(1) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..1776

(1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1) ANTI-SENSE: NO

(1) HYPOTHETICAL: NO

(1) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1072:

AAGATTATT GCATGCATAA TGGTATTAT GCGGCCACAG GGGCAATGG TACACAATTT
AACCGCTTGG ATTACCTC TAACAAATTA GCGAATTTA GCGAATTTA GCGAATTTA
120
180
240
300
360
420
480
540
600
660
720
780
840

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1071

(1) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..819

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(16) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(17) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..1131

(2) INFORMATION FOR SEQ ID NO:1074:

GTGATTTTAA CGTGTATCTT TCTAACCCCTA TTAATAATGTA TTTGCGCAGC CAAAAACAAG
CAGCGCGTCA AAAAGCCACC AACCAAGATCC ATTCAGAGTC TGCATAAATAT CACGCAAAAT
ATCCCCCCTC AAGTATTAAC CCGTCAAAATC CAGCGCGGTA TACAGAGGCT GATGCAAGGT
TTTGGGGGCTT TGAGCAGCAC TTGAGAACCC CCTTATTTGT TTTCTAAGCA AAATGTGCTG
ATTGGGGGCT TTGAGCATTA TTATTCCTCT TTATATGGGT GGGGCAAGAT TCACGATGCT
GCGCATTGCC GAATGGAATG CAAAAAGAGC CCAATGAAGT GTATCGCT

60
120
180
240
300
348

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1073

(17) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..348

(16) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(14) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1073:

ACTTATAGCT GGAACCTTT CTAGCAATTT TTGAAAAAG ATATTTTAA CACGCCCTAT
AAATTAAGAG TCAATTAACG TACTGAGGGG GCGCCTAGGA TTAAGGAGC TAAAGAAATG
CCCTTTAAG AAGTGTCCGA AAAATAGAC AAATCCAGC CAAGCCCTC TATCAATCTT
ATTATATCCA CCCATCAGA ACAGCCTTAA AATTTAAGA TCGCCAGAG AAAATGCCGA
GAGATCATCA ATATGCCCA TGAGAAAAA AGCCAAGTTG AAGAAGCCTT TTTAAGCTG
GCAAGATTTT TAGAAAAAGT GGAAGGCTT CATGAAAAA ACAATTAAG AGAGTTGAT
TTGAGAGAT TAGAAAAATT GAGCGCTGAA ATGATTAACG TTAAGAGCT TTTGATGAC
AAACGATTA ATTCGTATTT TATGATGCG ATACAATCTT ACATTTCCA CACGGAATTTG
CATATCGCTG AATCCGCTG TAAAAAAAG AGTAATGAAG ACGGATTAAG GGTAAAGCAA
TTGAGATACA TTATCGCGCA CAATTACTCG CTTTTTACGT TAGCGGGTGG GATGGAATTC

1200
1260
1320
1380
1440
1500
1560
1620
1680
1740
1776

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1076:

ACCTTAAAG GAGTGTGTTT GTTCAGATG ATAGGCGAT GGGTTTACA AGACAAGTTC
TTGTTGTCG TGTTTTTAT ATGCGCTTTT TGTTAGGGG TTTAGGCAC GCAATCTTT
AAACAAGACA CCCAAGACA GCTCCCTATC GTGTGTGTGG ATTGGATTA GACCACTACA
AGCCATCAAG TGCGTTTGA ATTAGGCGCA ACGAGTGTGG TTGAATCAA ATACCAAGTG
ACTAGGCTTT CAGAAGCTTA ACGCTTT

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1075

(1) NAME/KEY: misc-feature
(B) LOCATION 1...267

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1075:

CCATGAAT TTTTAAAT CCTTTAAT GAGTTAAG CCATTGTTT TCATTAAGGC
GTTTATTA TGCTTATAG CGCTCCCTTA ATCTATAGCT TGTTATACCC TTGCGCTTAT
TTGAAGAACA TCGTAACGCA GCAAAAAATC GCCCTTGTAG ATGAAGACAA TTCTTTAGC
TCTAGGCAAT TAGCCTTCAT GGTGCAAGC TCCAACAGT TAGAATTCGC TTCTTTAGC
CCCTATAG TGAAGCCAA AAGCCTTTTA AAGAAGAA AAATTATAG GATCTTACAC
ATTCCCTCTC ATTGGAAG CATATTTAT AAACAAGTGC CTGTAACGAT AGATTTTAT
GCGAAGCCA ATTACTTTT GATTATAGGT GCGTTAGCA ATCGGTGTG GGGGAGCATC
AAGCCCTTAA ACGATGAAT CAGGTTCAAA CGCAAGCCC AATAGAAGA AGCTGAATTA
GGGACAGAC GATTAAGAT TAAGCCTTAT GCTTGTATA ACCCTAGTGA GGGGTATTTG
AATTACGCC TCTTAGCGGT GTTTATTTTC ATCTTACACC AGGTGATGCT CATTGCAAGC
AGCATGTTA CTAGCTCCAG CGCTTGGAA TTGCGCCCTT TAGACAAGAA ACAATTCGCT
TTAAGGCGCT GCGCAAGACT CTGCTGTGTT ATGCGGCGGT TTAGCGTTT TGTTTATG
TATTTGGCG CGCTGTTTT TTTTATAGG ATCGAAGCGC TTTAATGTG TTTAATGTG
TTTTGAACA GCTTGATTT CATGCTTGG GCTTGAAT TGCGTGTGTT TTTAGGGGCA
TTTATGATG GTTTGTGTG GCTTTTGA TCGTTGCCCT CTATTTTGA AGTCTTGTGTT
TGATCAAAA ATGAAGCCCA CACCACTCAA ATCGTTTGA TTCTTCTTT GCCCTTGAT
TTTATGATG GTTTGTGTG GCTTTTGA TCGTTGCCCT CTATTTTGA AGTCTTGTGTT
CAATTAAGC CTGCTTATCA TGGGATCAGT TTGCTCGGCG GATTATTTAT CGTGAGTTT
GAATTATAG ATGTTATAT CCAATTTTAC GCGCTTATG CGCTTATG GTGAAAAAGC T

(1) SEQUENCE DESCRIPTION: SEQ ID NO:1074

786

SUBSTITUTE SHEET (RULE 26)

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(4) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

60 GTTCCGCAAT GTGCTTTGAG GCGTTTGGC GCGTTTGGC GTTCCGCAAT
120 GATTATGAG CAACCGGATG TAAGGCTCTT GTAAAAAGTT GTGCGGCTTG CCATGGGGTT
180 AAGTTGAAA AGAAGGCTTT AGGTAAAGC AAAATCGTTA ACATGATGAG CGAAAAAGAG
240 ATTGAAGAG ATCTTATGCG TTATAAAGC GTGCCAACA AGAATCCCTGT CATGACCGCG
300 CAAGCTAAA AATTAAAGCG TGAAGCATC AAAGCTTTAG CCATATACAT CCCCACTCTC
303 AAA

(11) SEQUENCE DESCRIPTION: SEQ ID NO:1077

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..303

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(4) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(2) INFORMATION FOR SEQ ID NO:1077:

60 ACCATGAAGA AACACACCT CTTTGATG GCTTATAT TCAATAGCTC TTAAAGCGCT
120 GTGATGGGA TTCTCAAC CGAGCTTCT TCTTTGAATT TGCTGTAAGA TAGCCCTGCT
180 TTGAACCAT CTACGCCCA AAACTCTCT TTAATAAGC CATGGAATAG GGTGTTGCT
231 AATCATGAG GCTTGATG CGAATAAG CCAATTAAGC AGCGAGTAA A

(11) SEQUENCE DESCRIPTION: SEQ ID NO:1076

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1..231

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(14) ANTI-SENSE: NO
(4) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078

AGACCTATGC TACATATAAA ATATCGTCCT AATGCTTGGC CCAATTATCAT GTCCCCAGAG
60
TACCTTACCA CATGCCAAGT TTTTATCGCT GAGCGGCATAG ACATTGTAAG GCGGTGCAG
120
TCCCCCAG GAGGCATTGA TGAAGGAGAG ACCCCTTTAG AAGCACTCTA TAGAATAATTA
180
CTAGAGAAGAA TTGGCAGCAA TGAATAGAG ATTTTGGCCG AATACTCTAG ATGATTCGCC
240
TATGATTTCC CAAGCAACAT GGAACATATA TTCTATTCTG TTGACGGGCA AAAGCAGCGT
300
TATTTTATG TCGCCCTTAA GCATGTTAAG AACTTGTATT TGAACAAACA CAGCCAGAGAA
360
TTAGATCTT ATCAATTCAT CCAGCTTAAG GATTGTCTTA AAAAATTCGT TCCCTTCAAA
420
CGCCAAGTGT ACCGCCAAGT CATCGCTTAT TTAGAAAAG AGGGTATTT GGGGTGT
477

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079

TCATGATAC TGTCCTTTT CTGGCCCGCT CTAGAGGCG CTATAGGAG CTCGTTAAG
60
TATTTGCG GCATATGAT GCCCAGTAA TTTTAAATGT TTGAAAGTT CCCTTTAAGG
120
ACTTTAGCG TGAATCTCAT AGGGTGTATT ATCATCGCT TTATGGGCA TTGCCCCCT
180
AAAAAGTTT TTGGGATGA TTTTGGGATT TTCTTTGTAA CCGAGTTT AGGGCGTTT
240
ACGACCTTT CTCTTATCG GTTAGACACT TTAACACTCT TGAATAATC CCAATACCTT
300
GAAGCCATT CTATGCTCT AGGACACTAC CTTTAGGGC TTATTTGGGT AGCTATCGGT
360
TGGTTTTGC CTAGAATTT TGTAGCGCTT AAT

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080

```
TAATTATCAA TCGTGTGGA AGATCAGAAA GGCATTTTCC CTATCCGACC GTCAAAAAGA
AAAGGCCAAA GCTCTGTGAT CATGGAAGAC GGTGTGCTTCA GCAAGAGAGA TTTGTAGAA
GGGCCAAAAG CGATTGAGGG GCTTTTAAA AAACATGCGT TTAAGGATTA TGGCATTAAT
TTTGGGCGATG CGTTAAGCCG GAATTGCGAC TTGTGCTGTA CGCCGATTC AGAAAAATGAA
CTGAAAAGAA AAGCGTTTGA AAATTAGTTT TCTGAGATGT TTTTAATGCT GAGCAAAAAGC
TCGTGCGCTCTA TTAAGCCGA ACATGGCCGA GGCAGGATGG TAGCCCTTT TGTGAAATG
GAGTGGGGAG AAAAGCTTA TAAGATCCAC AAACAATATC AGGAATTTGT TGATCCTTAAT
GCCCTTTTAA ACCCTGATGT GATCATCACA AACGATTAAG AAATCCACAC TAATAATTTA
AAGAGCATTT ACCCTATTTG AGAGCATTTG GACATGTGCA TGGATGTGG GTTTGTGAA
AAGCTCTGCG CCAGTAAAGA TTATATCCCTTA ACCGCCAGAC AACGCATCGT CATCCACAGA
GAGCTAGAGC GTTGAAGA AGGCTAAGT CATGGTCAATG ATGAAGATCA GTTTACTA
GATGAGCTTT TAAAAGATC TGAATACTTA GGCATGCGCA CTGCGCGGCT GTGCCATATG
TGTTCCACTT TATGCCCTTT AGGATTTGAT ACCGGGAGTA TCGCTTAAA TCATTAATCA
AAAAACCTTA AAGCGAAA GATCTGCTTC AAAGATTCT
```

(2) INFORMATION FOR SEQ ID NO:1081:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(16) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081

```
CGATTTTAC AAAAGAGTC GCAATTTC GCAATTAAA TCGTAGTA AATAGAGAT
TGACTAAA CTATGAGG TTTAAGCG CTAGACAATA TCAGTTGAA ACTACCAA
CAGCAATTA TAGGGCTTT AGGCCCTAAT GGGCGGGGTA AACCCACTCT GTTAAATTT
TTAGCCCCGAT TGAATTTGAA CTATCAGAGG GAAATGAAAA TTTTAAACCA AAGATTTGCT
AATAGAGCTA AAAAAGCGT GCGGTTTTTA AGCGATGGCG ATTTTTTGA TCCTAATTA
ACGCCCTTAA AAGCGATCGC TTTTATAAG GATTTTTTGA GCGATTTTGA TGAATCAAAA
GCCCTAATTT TGTAAAAACG CTTCACCGTG CCTTAAAAA CAGAGTTCAA AGCCCTTTCA
AAGGCATGA GCGAAAAATTT GCAGCTGATTT TTAACCCCTAT CACGAACCGC TTCTTTGTAT
CTTTTGATG ACCCGGTGGC TGGGATGAC CCTATGCAA GAGAAGAGAT TTTTGAATTA
ATCGGCTTACG AATTAGCCA AAACGCAAGC TTGCTAGTCT CTACGCATTT GGTGGTGAT
GTGAAAAAGT AATTAGACG CGCGATTTT TTAAGAAGAG CTAAAGTGGT GCGTTTTGGG
GATGTGGGG AATAAAAA AGGTATAGC AGTTGGAGG CAGCGTATTA AGAAAAGTTG
```

(2) INFORMATION FOR SEQ ID NO:1082:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(17) SEQUENCE DESCRIPTION: SEQ ID NO:1082

AAATCGTGT TTCTATGC CCTTTTAT GTTTGCTT GTTAAATAC CCTATCAT
GGCATGCGA TGAAGAAA AGCAAAAGTC TTTTGCTGTT GTTAAATAT GATTCGTTGG
TTGATTTGG CGGTCGTTT TTGTTGACG GTATGAGACG CTAAGAAAT CGCTATGCAA
CGATTTGACA AACAAAACA TAAGATTTT GAATCCCTTG CGATTAAGT GAGCGCCAAA
GACATATGTA TAACCGCCCTC AGGAATGCG ATCTATGTA ATATGACGT GTATATCTA
GCGGATGAG TCGGTATGA CACCAAGACT AAAGAAGCGT TATTAGAAGG CAATATTAAG
GTTATAGGG GCGAGGCGCTT GCTCGTTAA ACCGATATG TGAATTTAG TTTGAACGAA
AAATATGACA TCAATTTTCC CTTTATGTC CAAGACAGCG TGAAGCGGAT TTGGGTGAGC
GCGGATATTC CTAGCGGGGA GGATCAAAA TATAAGATTA AAAACATGAG CGCTTCAGGG
TGCAGATTC ACAACCCCAT TTGGCATATC AATGCGACTT CAGGCTCATT TAACATGCAA
AAATCGCAT TGTCAATGTC GAATCCCTAG ATTAATGTCG GCAATATTC IGTAATGTA
TTGCCCTATA TTCTATGTC CAGAGCAAT AAAAGAACTA CCGGGTTT ATACCCGTAG
TTGGCACTT CCCATGAG CGGCTTATTT TATTGCAAC CCTTTTATTT AGCCCCCAAA
AACTATGGG ATATGACCTT TACCCACAA ATCCGTACA AAAGGGGTTT TGGCTGAAT
TTTGAAGCGC GCTACATCA CCTT

(2) INFORMATION FOR SEQ ID NO:1083:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(15) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(17) SEQUENCE DESCRIPTION: SEQ ID NO:1083

ATCGTTAGAA AGAAGTAAAT GTTAGAGATG AGTTGCAAG CATTAATAAC ACAAGATTCT
TCTGTGATGG CTCATCCCTT GCTTGTCAT GCCTTTTTC CCGCCTTCT CCGCCTAGCC
TTTATGATCA ATCTTTACAC CCTTTTAA CCTTTTAA GAAAGAAAT TCATCCCAAT GAACCGGAAA
ATCTATCTTG TCATGCCAGC GATTATAT CTTTAAGCA TCGCTCTTTT GAGTGGGGTT
TTTATTTGGG CGATGCACA ATTTGAATTT TCTTTAGCG CTGTGTCAT GCTTTGGGG
TTGTGTGTA TGCCTCATGC AGAATCAAA CGCCATAAA GCGTGAATT CGCTATCACT
AAAAAGAAA GATGAAAGC CTATATCAAA AAAGCTAAA TCCTGTATTT TTGAAGAACG

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60 AAAAGCCTTA TCGTTTCTT TCTATCCATT TTTAAAAA GCTTAAATGA TTTTAAAGC
 120 GCTAAGAAATGC TTTTAAATCA TCTTGGCCCT ATCCTTTGA GTTGGCGCTT TTTTGAAGCT
 180 ATCTTTTAT ACATAGCCCG GAGTATGTG AATTATGCC AAACCTTAT ACCGCAATCT
 240 TTGAATGATT ACCGTCATTC TCAAGCGCTT TTGCGCGTGT TGTTCGCATG GGTTTTAA
 300 GCGTTAGTGT ATTTTCTTAT TTTTGGATC GTATTCCTTT TGAAGTTAGT CATCAATAT
 360 TTGCGCTCTA TTTTAAAC CCCTTATG GTCCTTAT TGCACCAAAA ATATTAATCCC
 420 CATGTCGTTT TGAAGAAT TGGCTCTATC CTTTCTTA TTAATATTT TTTAAAAATCG
 480 CTCACCTTTA TCGTTTAT TCTAGCGGTT TTAAGCCCC TTATTTTCAT TCCCTTATA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1085

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...705

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1085:

60 CCAGAAAGAG GGAATGAAT CAATGTGTT GAGCCGGTTA TCGCTTACAA GCTTTTCAT
 120 TCCTTTGTGA TTTTAAAGGTG CCGGATGAA ACTTAAACGA CTAAATGCGT GGAAGGCATC
 180 ACCGCTAATG AAAAGATTTG CCACGATAT GTTTTACAA GCATTGGCAT TGTTACCGCG
 240 CTCAACCCCT ATATCGGCTA TGAATAATCC GCTATGATCG CCAAGAAGAG CTTAAAAAGC
 300 GATCGCTCTA TCTATGAT TCGTTAGAA AGAATAATCT TAACCAAGA GCAACTGGAC
 357 GATATTTTCA AGCCAGAAA CATGCTAAG CCTCAGCGTT TCAAAAAACA TAAAGAC

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1084

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...357

(1x) FEATURE:

(v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO

(11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1084:

ATTCTATCA TCGTGTAT GGCAT

540 GGGGCTTTC GGGTCTTTT TCTTATAGTC CCGCATTTCC TCTTTTCAA AAACACCATC
 600 AGTTTGATA TACCAAGCAT GATTTTCAAC CATCAAGCT ATCAAAATTT ACTCAACAG
 660 CACCGATTGA AGCATATGCT TTTTTCGTTT TTTTGCATC TTTTTCCTT GATTCCTTTT
 705 TTTAATTTT TTGCCACCTT GTTGCACACC CTAATGTAA CGCAC

(2) INFORMATION FOR SEQ ID NO:1086:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...831

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1086

60 GAATGTAAG GAATGGAAT TATGAAAAG TTGTAGCTT TAGGGCTTCT ATCCGGCGTT
 120 TTAAGCTCTT CGTGTATAG CGAAGGTGAT GTGTATTATA TAGGGACTAA TTATCAGCTT
 180 GACACAGCCC GTTGAATAG CATATTTAT AATACAGGGG ATTGCACAGG GAGTGTGTA
 240 GGTGCCCCC CAGGCTTAC CCTAATTAAG CATATTCAG GAGGCACCAA TATCAATTGG
 300 CACTCCAAAT ACCGTAAATG GCGTTTGAAT GCTTTGGGT TGAATGTGGG TTATTAAGAA
 360 TCTTCCAAAT TCAATCGCT AGATATGACA AGCAAGTGGT TTGGTTTAG AGTGTATAGG
 420 CTTTGAAT ACCGCCATGC GATTTAGGT TGAACAGTTT ATGCACCTAA TAAATCCAG
 480 TTGATATGG TCTTTGGGG TGTGGGAGC GATTGTTAG CTGATATTAT TGATAAAGAC
 540 AACGCTTCTT TTGTATTTT TGGTGGGGT GCTATCGGG GTAAACACTG GAAAAGCTCT
 600 GCACCAAACT ATTGAAAAGA GCAATCATTT GAAGCCAAAG GTCCGTGATGT TTGTAAGCCCT
 660 ACTTATGTA ACCCTAATGC CCTTATAGC ACCAACAATT CAACCGTCCG TTTTCAAGTG
 720 TCGTGAAT TTGGGTGAG AGCCATATC TACAAGATA ATGGCGTGGG ATTTGGCGTG
 780 AGAGTCCCG TACTATCA TAAATTTT AGCGCGGCTC CTAAAGCTAC TAACCTTAT
 831 TACCATTTGA AACGGATTA TTCCGCTTAT TTGGGTATA ACTACACTT T

(2) INFORMATION FOR SEQ ID NO:1087:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2028 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2028

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1087

GCTTTGAGC AATTAGAGC TTGAGATTT TCCTCAAT CCCTAAGG GCGTGCAG
 60
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 120
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 180
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 240
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 300
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 360
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 420
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 480
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 540
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 600
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 660
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 720
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 780
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 840
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 900
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 960
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1020
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1080
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1140
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1200
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1260
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1320
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1380
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1440
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1500
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1560
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1620
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1680
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1740
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1800
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1860
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1920
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 1980
 AGTTGAGC AATTAGAGC AATTAGATTT TTAGATTTA TTAGATTTA
 2028

(2) INFORMATION FOR SEQ ID NO:1088:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(141) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(14) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION 1...828

(141) SEQUENCE DESCRIPTION: SEQ ID NO:1088

GCGGCTTTG TTAATACAC AGCGGATTT TTTTCCCTA TGAATAACGT GTTTTACCGC
 60
 TCATTAACA TGAAGCTTT ACTTCTGCT ATCTATCCT TCAAAACCTA CCGCTTGAAG
 120
 AGTTACAAAC AAGCGGCTTT TAAATAAGCT CCGTTAAGG TCGTTCTGCG GCGCTTACCG
 180

794

ATCGTGGCGG TTTTATTA TATTGAATAA ATTTCGCTCC CCACAGCGAA CGCTTCTCA
240
CAATGCGCGG CTATTATAC GGTGCTCTCTT TCCCTTTTCG TTTTGAAGA AAAGCTCAAA
300
AGAAAGCGCGG TAATTTCGCG ATGCATCCGGG CTAGTGGGGG TGGTGTGAT TTCAGATTCCT
360
AGCGTGGAAT ATGTAGAGAT AGTTGAATC ATTTAGCGCA TATTGAGCGG GATCTTTGTC
420
TCTTTAGCGG ATATCACTT AGGATTTG AGGAATAT ATTACGAAGA GCGCGTGAT
480
TTAGCGTTCG CTTTGGCAT GAGTCTCTT GATTTAGCGG GCATGTTCAT TGTATTTCCT
540
TTTATATCA CAGCGCTTCA TATCCCTAGA AAAGAAGATA TTTTAGAT TTCTTTAATA
600
GGATTTAGCG GGACTTTAGG GCAGTATTTT TAAACCTATG CTACATGAAG CGCTCCTGCT
660
GGATCATACG CCCCATTA ATACACCCCG ATGTGTTGGG GGTATTGTT TGGGCTGTAT
720
TTAGCGGATA CATTTTGGA TCTTAAAGC TCTTTAGCGG TGGCTTGAT CTATTGTTCA
780
GGCTTGTCTA TTGCTTGGC CGCTCTTTTA AAGAATTA AAAAATT

(2) INFORMATION FOR SEQ ID NO:1089:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(16) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(16) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1..807

(16) SEQUENCE DESCRIPTION: SEQ ID NO:1089

GTGATGCAC TAAGCCCTT ACAAGCGCG CTGTATAT TCCGTACTT TATTATCCG
60
GAAAAAATA CAAGAGCTT TGAATTAAG GATTATAT TATTGAT GGTTTTAT
120
GTCTAGCTT TGGGCGTGT GATGAGCGAA GAAATTTCTA TCAGCTACAA TGAAGCGAAA
180
GACTTTTTT ATAGCGATG GTGGTTGTC AAAATTCGCTC AAAAAGCGGT AGCCATTTTA
240
GGCCAAAAG ATTGCGCTT AGATTTGCT TTTTGATCG CTCACGTCA CACATGTCTT
300
TTATCTTACC TCATAGCGG AAGATTTTA AAAAAAGCTA AAGACGCTCT TATGTGTGTA
360
TTGACTTACC CTTATTTGCC TGGGTGAT CTCTTTGCGA TTTTACTGGC TAAAAAGCGTG
420
CTGTGTGTTA GCGTTGGCT TTGATTTAGC TATTGTATA TTAAAAACCA AAAAATCCCT
480
TATTTAACCC TTAGCGCTTG CGCGTTTTA GACGGTGGGT TCATCCCGCT TTACTTAGGG
540
GTTTTGCCCT AGCGTTAAG AAACCGCTAT TTAAAGAGCG CGATCTTTCG TTGGTGTGTT
600
TTAATTGTGA ATACCGCTCT TTTTAGTGGG GATTTTATA AAGGCTTGGC TAGCGGGTAT
660
TTTATAGACA CTGCTTAGA ACTCATGCTT TGTATTTGCG CCTTATTTGTT CCTTACTAC
720
CCTTATACG TCTTAAAGC CTTTGGAT AAAAAGCAT CGTACTAGC CTTATGCGG
780
CGAGCGGCTG TTTTCCCT TTGCTTT

(2) INFORMATION FOR SEQ ID NO:1090:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature (B) LOCATION 1...723

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1090

AGCCCTTTA TGAATGAA ACTCTTAA TATATCAAG CCTTAAACG TTAATCTTAC
 AATAGCGATT CGCTTTTAT ATACGATTT TCACGCCCTT TATCAAAA TAGCGCGCGG
 ATTTTACAC TAGCTTACAG GTGTGGGGT CTAGGGCTTG TCTGCGCTTAG AGACAACCCG
 CTAGCGGCGG TTAATTTTAT GGAATAAGAT AGCAATAATG CGTTTGTCTC CCAAAAAAAC
 GCCCTTAAT TCCCTAACGC TCAAGTGTAT GAGAGCGATT TTTAAGATT TAACCCCTCCG
 ATTTTATAT ATGCGATTGT GTGCAACCCG CTATTATATG CTTAAGATC TATTAAATCT
 CAATTAAAG GCGATGCCAG GCACCAAGC GAATTAGACT TCGCTTCTTT GTTGGCTTAA
 GTGAATAAT GCCTGAACCC TAAAGGGGTAT TTTATTTT GTATGAAGC CTGTGTGCTT
 TCGTTGTCA TAGACAGCTT AAAAAGCGT AAACCTACCG TAGAATCTT AAGCTTTGTC
 CAAGTTTCA AAGACAAAA CGCCCATTTG ATGCTTGAAG CGGCTAAGAA TAAATCCAAA
 AGCGCTCTTA AAGTTTGGCC CCTTTAATC ACGCACAAAT CCAAAAAACC AAGCGACAC
 ACCAAGAAAG TTTAAACAT CTATCAAT TGTAAACACT ATCTATCAAG AGCGCCCTTA
 GAT

(2) INFORMATION FOR SEQ ID NO:1091:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature (B) LOCATION 1...1287

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1091

TCCTGCTCTT TTAGGGGGCT ATTATATAT ATTAAGATTA ATTGATTA TAAAGATACA
 GCGTTGCAAT AAGATTAAT AGACATTTAG GCCACTTTAG TGTGCATGAT TTTGGTGTG
 CTTTGGGGC GTATGTGAT TTCTAAGTC AGCTTAAAGT TATATCAATG TAGCGCGCTA
 CTTGTGTGAG GTGGGGTTT AGTGGCTTT TTTATCAATG TAGCGCGCTA ATTTTATCA
 TTGGCTTGC AGTTTGATC TTCTTAAA GATCCCTTAA TGTGACTTT CTTCATCAC
 ATTGTTTCA GCGCGGATTT CAATCTTTA CAATAAGCGG GGAATAATGCT TCGCGGTTT
 TTGCTGGCTG TACGGGGGTT TGTGTGTGTC CAAAATGTCAG TGGCGATTTC TATCGCTA
 CTTTAAAGGG TCAATCTCTT AATCGGGGCT TTAGGGGAT CGATCGCTTT AGTGGGTG
 CATGGCACTA GTGGGGCATG GCGTAAATTT TTCACCCAAC CACTTATCA TTTAGCTCT
 AGCTTGGAAG TGGCCATGCG GTGCGCGACT TTTGGCTTGG TGAAGCGGGG GATTATGGA
 GGGCGCTGCG CTAATATTTT GATTTCTAAA TACAACCTAG AACCTAAGAA CACTAAGAA
 AAGACACTT TAGAGGGCGT CGTGTCTAAA GGTTTGAAA CCCCTAAGAA GCAGCGCGCTA
 ATCACTGCAT CCAGTTTGTG AGAATCTTGA GCTTCTCATG CAATAGCTTT ATTAGTGGG
 ACTTTTAT CGCATTTGAT GCCTAAAGT TTCACTTAC CGACTTTGCT GTGGTGTG
 TTGTGGGGG TATCTTTAG GAACCGCTTG TCGTTTTTA AAATCCATAG CGTGTGTGAC
 AAGAGAGTTT CAGTTATAGC GAATGTGAGC TTAAGTACG GTTAAACTC TTTAGCTTA
 AGCGTGAAT TATTTGGAAT GTTAAACTC TTTAGCGCTT TTTGAGCGTT TTTGAGCGTT

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1093

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1323

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(A) LENGTH: 1323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1093:

AAATTCGTTT TCGCTCAAT TCAAGATA AAGATGCTTT CAGTGATGA AAAAGGGAAT
GCCCTAGACA AAGAGGATGCT TGAAGAAATG CTTTAAAGCG AAGACATTTT AATGGAATAAC
GCCCTATAGC CTTTAAAGAG GCGCGTTTAA CATAACGCTT CTTTGGGCGC TAAGGTCATT
ATTCTTTGTC GAGTGGGGA TAAATGAGGT GATGCTTATA CTCTAGCCAG GCGTTTATG
GGCGCTTTTA AAACGCTGCT CTTTGAATG AAATTAAGCA AAAGCCCCCAT GTGCCAATTG
CAAAAGAAA GCGCTAAAAA AGTAGGGGTA GTCAACAAG CATGGGAGA AAAGAATGAA
GATTAGAAAT GCGATGTGTT AGTAGATGCG GCGCTTTTAA GCGCGGATTA GCGCGGATTA
GAGCGCTTTT TAGATTTTGA AAGCCTTCT CAAAAAGCAC GCTTAAAT CGCTTGGAC
ATTCCAGCG GATAGATTC TAAAGGCGAG GTGATTAAGA GCGGTTTAA GCGGATACGA
CTATCAGCAT GGGCGCTATC AAGTCATGCT TAC

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1092

(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(ix) FEATURE:

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(iv) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: DNA (genomic)

(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1092:

CAAGTGGCGG TTATGATCCT TTATGTGTC CTCTAACCT TTAGGTATG CCGGAAGAT
TATGATGCGG CGGTGTGTC GCGGGGAGT GCGGTGAGC GACCCCAACG GACCCCAACG
GCTATGCTGA ATATGCAAC CATCAACCAAC CATATGCGG CATCGCATGT GCGGTTATC
GTGCGCCCTT TAGTGGAGC GTTTTGTG GATATTTATTA ACGGTTTAC GATTAAAGGC
TTTTGCTTT TGCCTTTT CCCTAGT

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GAGCGCTTAA ACCCGATAC GACTATACAG ATGGCGCTTA TCACTCATG CTTACTAAGC
 60
 120
 180
 240
 300
 360
 420
 480
 540
 600
 660
 720
 780
 840
 900
 906

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1094

(1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1..906

(v1) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (1v) ANTI-SENSE: NO

(111) HYPOTHETICAL: NO
 (11) MOLECULE TYPE: DNA (genomic)

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 906 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(2) INFORMATION FOR SEQ ID NO:1094:

AATGCCACAA ACTTGAAAGA TAAACCTTT CAGCGCGGCT TTGAACCTCT TACAGCCCCC
 60
 120
 180
 240
 300
 360
 420
 480
 540
 600
 660
 720
 780
 840
 900
 906

(2) INFORMATION FOR SEQ ID NO:1095:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..1125

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1095

CTCGCTTAC GCTAAAGC GACCGGTT CCATTCCA AAGTGGCTAC CATGCTTCCG
 CTAGGTTT GCTAGATG AATTAAAC GATATTCA ACATTTGAG CATTGCTG
 CCTAGTTG ATTAATCG GTGAAAAA CCTGCTTG ACATTTGAG CATTGCTG
 GTTCTAGCA CTTAGGGAC TTCCATGAAA AGCATTTGAG AATGATGCG
 GATTAGGGGG GATTAGGGGG GATTAGGGGG GATTAGGGGG GATTAGGGGG
 AATTCTTAC AAGCTTAC AAAAGCGTTA TGCTCTTTG AAAACAATTG GCTAGGGTT
 GAATCGTTA GCAAGATT AGAGGCGGTA AAAAGGAAA TCCGCGCGCC CAATCCCAA
 CGCTGCTCT ATATTGCTA TGCGTTGAG TTGGCGGTT CTGTGATGA AGTGTGAA
 TTATGCCAG TTGACAGGT GTTTTATCT CAATTCAA AACTAGTCA AGCAGAAG
 GGCATCAAT CTAGCGTT AACGAGCGCC AAAAATTTGA GAGGCGTTA AAAATTTAGC
 TTAGCGATG CAGGATTC CACTAAATC AAAGAAATG AAAATTTAG GGTCAAGCCT
 TTGAAGTG AATTAGCT ATCTAATT CAATCGCGC CCATTTTG AGAAGTGCAC
 ACTGCGCGC CGAGTTT ATCGCTCAG CCTAATTGT ATCCCACTA TCCCCCTAAC
 CCTTGGCCC CTATTGAAA CAACACAGAA AAAAATCTT AATCATAGC
 TCTGGGCTA ACCGATCG TCAAGGCAAT GAATTGAT ATGTGCGT GCATGCGAGC
 TTGCTTTA AAGATTGA CATTAAGC GTATGCTCA ATGCAATCC AGAACCCTA
 AGCAGGAT ATGATACTA GTATACGCT TATTGAAAC CCATACATT TGAATGTG
 AAGATATC TTCAAGGGA GCGATTTG GCGATTTG TGCATTTG GGCACAAC
 CCTTAAAC TCGCTAAG TTAGCCCAA ATGCAAGCCC CATTTATG CACGCCCTTT
 AAGTGAATG ATATTGCGA AAATTTCCCT GTTT

(2) INFORMATION FOR SEQ ID NO:1096:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(1x) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..456